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Result
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Listing first 45 summaries
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1: sp_archea:*
2: sp_bacteria
3: sp_fung1:*
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Match
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90.6

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Gapop 10.0 , Gapext 0.5
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sp_rvirus:*
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 ij
Q9ZT62
Q9YWN6
Q9YWN6
Q942T6
Q9SBZ0
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11.9	11.9	12.1	12.1	12.1		12.1				12.2													18.5					37.8
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Q26960	Q9ABL5	Q9DJV1	Q8TWT1	Q98VM4	Q9BT41	Q911Y7	091632	Q9P938	Q8TAP0	Q9NUX3	Q9S377	031962	064059	Q497.99	055716	804460	Q970S3	Q9PN62	Q9LN46	Q94W95	Q9ZCM8	Q9FVM2	004607	Q39466	Q93CM6	Q96XG2	097094	Q9LFZ7
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ALIGNMENTS

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Matches 101
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Q9ZT62;
Q9ZT62;
Q1-MAY-1999 (TrEMBLrel. 10, Created)
Q1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
Q1-MAY-1999 (TrEMBLrel. 20, Last annotation update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                     TISSUB-LAAR; Ohsumi C., Nozaki J., Kida T.; Ohsumi C., Nozaki J., Kida T.; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases. Submitted (JUN-1998) to the EMBL, AF073744; AAD02832.1; -. EMBL; AF073744; AAD02832.1; -. Glycosyltransferase; Transferase. Glycosyltransferase; Transferase. 3B06A491F0908933 CRC64;
                                                                                                                                                                                                                                                                                                                            Cucumis sativus (Cucumber).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
 Q9FND9
                                                                                                                                                                                                                                                                               TISSUE-LEAF;
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                                                           TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR 101
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 PRELIMINARY;
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Pred. No. 1.7e-54;
 PRT;
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RESULT
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Matches 90
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                                                                                                                                                                                                                                                                                                                                                                                                         Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Sakurai T., Theologis A., Davis R.W., Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AN08702; BAB11595.1; -EMBL; AN08702; BAB11595.1; -EMBL; AV081645; AAM102071.; -EMBL; AV081645; AAM102071.; -
                                   Pisum sativum (Garden pea).
Eukaryota; Viridiplantae; Strej
Spermatophyta; Magnoliophyta; e
eurosids I; Fabales; Fabaceae;
                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence up
01-MAR-2002 (TrEMBLrel. 20, Last annotation
Raffinose synthase (EC 2.4.1.82).
SEQUENCE
                                                                                                                                                 Q8VWN6;
01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structural analysis of Arabidopsis thaliana c
Sequence features of the regions of 1,044,062
physically assigned Pl clones.";
DNA Res. 4:291-300(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2002 (TrEMBLrel. 21,
                      NCBI_TaxID=3888;
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89.1%;
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                                                             Streptophyta;
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Pred. No. 1.5e-48;
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                                                 eudicotyledons; core e
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                                      Papilionoideae;
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2 bp covered
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                                     core eudicots;
vicieae; Pisum
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                 Q9SBZ0 PRELIMINARY; PRT; 857 AA.

Q9SBZ0;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2000 (TrEMBLrel. 20, Last annotation update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Phaseolus angularis (Adzuki bean) (Vigna angularis).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot
eurosids I; Fabales; Fabaceae; Papillionoideae; Phaseoleae;
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01-DEC-2001
01-DEC-2001
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Q942T6;
                                                                                                                                                                                                                                                                                                                                                                Submitted (FEB-2001) to the EMBL/GenBank/DDBJ EMBL; AP003282; BAB64768.1; -. SEQUENCE 816 AA; 89588 MW; B316EDF3566C51
                                                                                                                                                                                                                                                                                                                                                                                                      "Oryza sativa nipponbare(GA3) genomic DNA, clone: P0583G08.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
MCBI_TaxID-4530;
        NCBI_TaxID=3914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (Rice)
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SEQUENCE 798 AA; 88717 MW; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-2002) to the EMBL/GenBank/DDBJ EMBL; AJ426475; CAD20127.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular characterization of raffinose synthase sativum L.) seeds.";
                                                                                                                                                                                                                                                                                                                                                                                                                                Sasaki T., Matsumoto
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV.
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1 Similarity 82.2%;
83; Conservative 1
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85
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Pred.
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Pred. No. 1.
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No. 9.
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                                    core eudicots;
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                                              Tracheophyta;
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                                    Rosidae;
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ID OBRX87

ID OBRX87;

AC Q8RX87;

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE AT5920250/F5024_140.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

C Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

Anirosids II; Brassicales; Brassicaceae; Arabidopsis.
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08RX87
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OC Euka
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PRELIANALISM
O93XKZ;
O93XKZ;
O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peterbauer T., Mucha J., Mayer U., Popp M., Gloessl J., Richter A.; "Stachyose synthesis in seeds of adzuki bean (Vigna angularis): molecular cloning and functional expression of stachyose synthase;. Plant J. 20:509-518(199).

EMBL; Y19024; CAB64363.1; -.

Glycosyltransferase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases EMBL; AJJ11087; CAC38094.1; .
Glycosyltransferase; Transferase.
SEQUENCE 853 AA; 95890 MW; CB10F18CBD37B38C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CV. WUNDER VON KELVEDON; TISSUE-SEED Peterbauer T.;
"Molecular cloning of a cDNA encoding for s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta; eudicotyledons; eurosids I; Fabales; Fabaceae; Papilionoideae;
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                                                                                                                                                                                                                                                                                                       PDWDMFQSDHVCAKFHAGSRAICGGPIYVSDNVGSHDFDLIKKLVFPDGTIPKCIYFPLP 642
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70; Conserv
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95890 MW; CB10F18C8D37B38C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptophyta; Embryophyta; Tracheophyta; yta; eudicotyledons; core eudicots; Rosidae; seae; Papilionoideae; Vicieae; Pisum.
                                                                                                                                                                                                                                                                                                                                                           11; Mismatches
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Pred. No. 4.4e-37;
"" matches 17;
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                                                               eudicots; Rosidae;
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RESULT 9
Q43408
ID Q434
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Q43408;
Q43408;
01-NOV-1996
01-NOV-1996
01-DEC-2001
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NCBI_TaxID=4513;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Arabidopsis cDNA clones.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AY090237; AAL90901.1; -
SEQUENCE 844 AA; 94215 MW; 2AC8AB0EA43F8056 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,
Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou I
Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                       imblbition in barley.";
Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases
EMBL; M77475; AA32975.1;
SEQUENCE 757 AA; 82133 MW; EA9E7B771AABBCCF CRC64;
                                                                                                                                                                                                                                                                                                                                                          STRAIN-HIMALAYA;
Heck G.R., Dorsett C.,
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01-NOV-1996
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                                                                                                                                                 61 TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR 101
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68; Conserv
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Pred. No. 2.6e
14; Mismatches
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Last sequence update)
Last annotation update)
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Pred. No. 2.9e-36;
                                                       PRT;
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              sequence
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annotation update)

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RESULT

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01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, L
01-MAY-2000 (TrEMBLrel. 13, L
Imbibition protein homolog.
  Q94A08;
01-DEC-2001
01-DEC-2001
                                                                                   Q94A08
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Brassica oleracea (Cauliflower).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae: Rraceica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EU Arabidopsis sequencing project;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL133248; CAB6610-1; -
SEQUENCE 773 AA; 85143 MW; 0852F9E67952C8D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thallana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embry.

Spermatophyta; Magnoliophyta; eudicotyledons;

eurosids II; Brassicales; Brassicaceae; Arabi
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Fujikura Y., Karssen C.K.;
"Cauliflower CDNA encoding a putative imbibition protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Benes V., Rechmann S., Borkova D., Ansorge W.,
Mayer K.F.X., Quetier F., Salanoubat M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases EMBL; X79330; CAA55893.1; -.
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                                                                                                                                                                                                                                                                                                                                                                       1 PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60
                                                                                                                                                                                                                                                                 TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR 101
                                                                                                                                                                                                                TRDCLFADPARDGISLLKIWNMNKFTGIVGVFNCQGAGWCK 578
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     (TrEMBLrel.
                           (TrEMBLrel.
                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.98;
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Last sequence update)
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Pred. No. 3
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Pred. No. 3e-36;
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3.9e-36;
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edons; core eudicots; Rosidae;
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Best Local
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                    Cicer arietinum (Chickpea) (Garbánzo).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; ddicotyledons; core eudicots;
eurosids I; Fabales; Fabaceae; Papilionoideae; Cicereae; Cice
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EMBL; AY050772; AAK92707.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ol-DEC-2001 (TrEMBLrel. 19, Last annotation update) Putative imbibition protein.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eeurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                        Submitted (JAN-2000) to the EMBL; AJ271668; CAB71135.1; NON_TER 1
                                                                                                                                                                                                                                                                       STRAIN=CV. CASTELLANA; TISSUE=ETIOLATED OSMOTIC Dopico B., Romo S., Labrador E.;
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                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3827;
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150
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                                                                              1 PDWDMEQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60
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TRDCLFVDPARDRTSLLKIWNMNKCTGVVGVFNCQGAGWCK 190
                              TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR 101
                                                             PDWDMFHSLHPAAEYHAAARAIGGCPIYVSDKPGNHNFDLLKKLVLADGSVLRAQLPGRP
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                                                                                                                                                                                            42180 MW;
                                                                                                                                            69.5%;
67.3%;
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66.3%;
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Pred.
                                                                                                                           Score 392; DB 10;
Pred. No. 1.3e-35;
1; Mismatches 22
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No. 3.9e-36;
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edons; core eu
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                                                                                                                                                           Length 386;
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Matches 68
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Matches 65
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Transferase; Glycosyltransferase.
SEQUENCE 863 AA; 95227 MW; DD96FE666099DEFD CRC64;
                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN-CV. HASS; TISSUE-MESOCARP;
ZBMOTANO J.P., Evans A.D., Dopico B., Lowe A.L., Wilson I.D.,
Merodio C., Grierson D.;
"Isolation and characterization of cDNAs for mRNAs regulated
cold storage of avocado (Persea americana Mill.) fruit.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ131148; CAB77245.1;
-.
SEQUENCE 779 AA; 85368 MW; C3A8B43160316785 CRC64;
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01-DEC-2001
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Spermatophyta; Magnoliophyta; eudicotyledons; core euc
Asteridae; euasterids I; Lamiales; Lamiaceae; Stachys
                                                                                                                                                                                                                                                                                                         Persea americana (Avocado).
Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Laurales;
                                                                                                                                                                                                                                                                                                                                                                                                                     Q9M4M7;
                                                                                                                                                                                                                                                                                              Spermatophyta; M
NCBI_TaxID=3435;
                                                                                                                                                                                                                                                                                                                                                                Putative seed imbibition protein.
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"Molecular cloning of a cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                 PDWDMFQSTHPCAAFHAASRAISGGFIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60
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TRDSLFVDPARDGVSLLKIWNMNKCLGVVGVFNCQGAGWCK 582
                                                  PDWDMFHSLHPAAEYHGAARAVGGCPIYVSDKPGHHNFELLKKLVLPDGSVLRARLPGRP
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                         TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR 101
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                                                                                                                    Similarity
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(TrEMBLrel. 15, Last sequence up
(TrEMBLrel. 19, Last annotation
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                                                                                                        Conservative
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                                                                                                                    67.28;
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68.7%;
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Eukaryota; Viridiplantae; Streptophyta; Embryo
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2000 (TrEMBLrel. 15,
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Huang E.N., Nascimento L., de la Bastide M., Habermann K
Preston R. R., Spiegel L.A., See L.H., Shah R., Matero A.
O'Shaughnessy A., Rodriguez M., Shekher M., Swaby I., Sc
Parnell L.D., Dedhia N.N., McCombie W.R.;
"Arabidopsis thaliana BaC T7B11 from chromosome IV near
"Arabidopsis thaliana BaC T7B11 from chromosome IV near
submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                         EU Arabidopsis sequencing pr
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EMBL; AC007138; AAD22659 1;
EMBL; AL161493; CAB80690.1;
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C96599
D90496
T09530
T01717
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trophozoite surfac
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Query Match 71.1%; Score 401; DB 2; Length 765; Best Local Similarity 66.3%; Pred. No. 8.1e-35; Matches 67; Conservative 13; Mismatches 21; Indels

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Gaps

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1 PDWDMEQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60

qui

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C;Accession: C85025
C;Accession: C85025
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold R;anonymous, 769-777, 1999
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C85025
                                                                   QΥ
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                                                                                                                                           QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein AT4g01970 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
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A; Introns: 64/2; 146/1; 176/2; 192/3; 223/2; 259/2; 300/2; 484/3; 507/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-773 <BEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the Protein S
A; Reference number: Z23014
A; Accession: T46188
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C;Accession: T46188
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N;Alternate names: protein T8H10.120
C;Species: Arabidopsis thaliana (mouse-ear cress)
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                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-807 <STO>
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                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                               A;Gene: AT4g01970
                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:NC_001268; NID:g7268581;
                                                                                                                                                                                                                                                                                                 Genetics
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Best Local Similarity
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                                                                       59
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                                                                                                                                               PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGK--HNFDLLKKLVLPDGSILRSEYYA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR 101
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                                    LPTRDSLFKNPLFDKESILKIFNFNKFGGVIGTFNCQGAGW 630
                                                                                                          PDWDMFQSDHVCAEYHAASRAICGGPVYLSDHLGKASHNFDLIKKLAFFDGTIPRCVHYA 589
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67; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rechmann, S.; Borkova, D.; Ansorge, W.; Mewes, H.W.; Lemcke, K.;
                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                   65.8%; Score 371; DB 2; Length 807 67.3%; Pred. No. 1.4e-31;
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                                                                                                                                                                                                                                                                                                                    PIDN:CAB80690.1; GSPDB:GN00140
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A;Gene:
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D90496
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RESULT
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Gene: SSO3127
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Best Local
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                                                                                                                                                                                                                         Local
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; De ansen, N.F.; Hughes, B.; Hulzar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; M. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Rosidues: 1-1170 <5TO>

A;Residues: 1-1170 <5TO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: D90496
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awa: Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein SSO3127 [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 2
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R; Theologis, A.; Ec
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
C96599
                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-649 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A99139
A; Accession: D90496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Description: Sulfolobus solfatarious
                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE006641; NID:gl3816550; PIDN:AAK43227.1; GSPDB:GN00155
                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
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                                                                                                                       1 PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKH----NFDLLKKLVLPDGSILRSEY
                                          YALPTRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGG
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PALITEDLLFKDPLRE-RVLLKLKGKVKGYNAIAFFNLNSG
                                                                                               PDYDMFMSYDPYAKVHLVARVFSGGPIYITD --- RHPERTNIELLRMAVLPNGEVIRVDE 511
                                                                                                                                                                                                    42;
                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                    Conservative
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Pred.
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Pred. No. 1.9e-14;
2; Mismatches 15
                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete genome
                                                                                                                                                                                                                            183; DB 2;
No. 1.5e-11;
55
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Maiti, R.;
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goc, H.P.; Red
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Redder
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A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: F70392
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submitted to the EMBL Data Library, June 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein A_IG002N01.5 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 24-Mar-1999
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C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C;Accession: T09530
R;Cervantes, E.
                                           A; Molecule type: DNA
A; Residues: 1-165 <AQF>
                                                                                                                                                                                                                                   hypothetical protein aq_1075 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May.1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: F70392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A; Accession: T09530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, February 1996 A; Reference number: {\tt Z16718}
                   A;Cross-references: GB:AE000721; NID:g2983544; PIDN:AAC07132.1; PID:g2983558; GB:AE00065
                                                                                   A; Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                      Nature 392, 353-358, 1998
                                                                                                                                                                                                                 R; Deckert,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:AF007269; NID:g2191126; PID:g2191156
A;Experimental source: cultivar Columbia
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A; Residues: 1-371 <SCH>
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    A; Experimental source:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local :
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A_IG002N01.5
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                                                                                                                                                                                                                                                                                                                                                                                                         PDWDISSSSWRMCHLC---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translated from GB/EMBL/DDBJ
                                                                                                                                                                                                             G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
23; Conserv
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25; Conserv
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strain VF5
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; Pred. No. 0.000
3; Mismatches
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Pred. No. 0.00
8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240/1;
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R; Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, I. C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, Nature 403, 665-668, 2000
A; Title: The genome sequence of the food-borne pathogen Campylobacter jejuni A; Reference number: A81250; MUID:20150912; PMID:10688204
A; Accession: E81330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: The genome sequence of Rickettsia A;Reference number: A71630; MUID:99039499; A;Accession: B71676
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A; Gene:
                                       A; Cross-references: GB:AL139077; A; Experimental source: serotype
                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-273 <PAR>
                                                                                                                                                                                                                                                                                 C; Accession: E81330
                                                                                                                                                                                                                                                                                                   C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-576 < AND>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Nov-2000 C;Accession: B71676
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                                                                                                                                                                                                                                                                                                                                               probable periplasmic protein Cj1235 [imported] - Campylobacter jejuni (strain
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;354-548/Domain: ATP-binding cassette homology <ABC>
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                    Genetics
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Best Local
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mes 28; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rickettsia prowazekii
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27; Conserv
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                                       GB:AL111168; NID:g69684444; PIDN:CAB73489.1; O2, Strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 75;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 76.5; DB Pred. No. 0.79;
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1, S.; Bar
                                                           PID: g696
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Query Match Best Local Similarity

12.6%;

Score Pred.

71; No.

5.6;

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Length

273;

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RESULT
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R; Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
submitted to the EMBL Data Library, November 1993
submitted to the EMBL Data Library, November 1993
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A; Residues: 1-212 <SMI>
A; Cross-references: EMB
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C;Date: 19-Mar-1997 #sequence_revision
C;Accession: S72873
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C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: The DNA sequence of Chilo iridescent virus between A; Reference number: Z14834; MUID:98141693; PMID:9482589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Bahr, U.; Tidona, C.A.; Darai, G. Virus Genes 15, 235-245, 1997
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                                                                                                                                                                                                                                                                                                                         A; Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S72873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein B2126_F2_70 - Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL: AF003534; NID: g2738385; PIDN: AAB94427.1; PID: g2738400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-959 <BAH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                 174 --- GWC 176
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                                                                                                                     95 QGGGWC 100
                                                                                                                                                                                                41 LKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFN-----C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
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                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 -TMLKIWNLNKFTGV 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRAISGGP-IYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFED---PLHNGE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GQKIKKGELI----GLSGATGRVSGPHLHFGILAGG 256
                                                                                                                                                          LRLIYLADSQLLD---YA-PDRDEL----LRFGKTLMAIWRTIQFSGETGDFRPNPSRLC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRMKTGEPYICFIDTCNKHMYDFQKKKGL---TIKQSNLCVAPETMILTEDGQFPIKDLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAFHAAS--RAISGGPIYVSDS----VGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLF 66
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                                                                                                                                                                                                                                                               12.5%;
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(20
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Nature 409, 1007-1011, 2001
Nature 409, 1007-1011, 2001
A; Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.;
A; Title: Massive gene decay in the leprosy bacillus.
A; Title: Massive gene decay in the leprosy bacillus.
A: Peference number: A86909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosonó, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seakeuchi, M.; Tamakoshi, A.; Tanamoto, H.; Yamane, F.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; A; Accession: F69912

A; Accession: F69912

A; Accession: F69912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: B87073
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A;Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Bacillus subtilis phage SPBC2
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999
C;Accession: T12810; F69912
C; Genetics:
                                                                                                                                                                       A; Reference number: A86909; A; Accession: B87073
                                                                                                                                                                                                                                                                                                                                                                                       R; Cole, S.T.; Eiglmeier, K.; Parkhill, R.; Davies, R.M.; Devlin, K.; Duthoy, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q
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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Alberlini, A.M.; Alloni, G.; Azevedo, V.; Beron, G.; Bron, S.; Broulllet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
                                                                  A; Molecule type: DNA
A; Residues: 1-294 <STO>
                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                             eam, M.A.; Rutherford, K.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved hypothetical protein ML1312 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
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A; Residues: 1-236 < KUN>
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C;Species: Bacillus subtilis phage SPBc2
                             A;Cross-references: GB:AL450380; NID:g13093231;
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A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: nucleic
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21.5%;
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Pred. No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                           , J.; James, K.D.;
S.; Feltwell, T.;
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                                 PIDN:CAC31693.1; GSPDB:GN00147
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Fraser, A
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 GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen Ltd.
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VN34_ROTPC
BBS2_RAT
                                                                                                                                                                                                                   YA75_AQUAE
SYE_AERPE
FLA3_PYRKO
                                                                                                                        Y083_NPVOP
TERT_YEAST
NIA_NEUCR
Y872_RICPR
API2_SOLTU
YC56_PORPU
                                                                                                                                                                                        MRAZ_TREPA
YJ9L_YEAST
PM17_MOUSE
TS11_GIALA
                           VPP_BPP2
RNP1_YEAST
MOTY_VIBPA
CELF_VZVD
PAP1_XENLA
                                                               HTR3_HALSA
VAA1_HUMAN
ROXN_HUMAN
YGN3_YEAST
DAP1_BACHD
CCPR_PSEAE
IF2P_PYRHO
RHOD_HUMAN
SOML_GADMO
DAPA_RICCN
                                                                                                          SUHB_BUCAI
HTR3_HALN1
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251.930 Million cell updates/sec
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9 pyrococcus
8 treponema p
5 saccharomyc
6 mus musculu
6 giardia lam
9 haemophilus
                                                                     porphyra pu
buchnera ap
halobacteri
halobacteri
homo sapien
homo sapien
saccharomyc
bacillus ha
                                                                                                                                       orgyia pseu
saccharomyc
neurospora
rickettsia
                            saccharomyc
vibrio para
varicella-z
xenopus lae
                                                                                                                 porphyra pu
buchnera ap
homo sapien gadus morhu rickettsia
                                                                                                                                                                                                                                  aquifex
                                                                                                                                                                  porcine rot rattus norv
                                                         pseudomonas
bacteriopha
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RESULT 2
SYE_ABERPE
ID SYE_ABERPE
AC 09Y9H1:
DT 30-MAY-2000 0
DT 16-OCT-2001

STANDARD;

PRT;

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(Rel. (Rel. (Rel.

39, Created)39, Last sequence update)40, Last annotation update)

Q ₽ Ş

Query Match Best Local S Matches 28

Similarity

13.6%; Score 76.5; 29.5%; Pred. No. 0 12;

Mismatches

22; DB 1; 36;

Length 165; Indels

19;

Gaps

9

Conservative

В

138 54 82

IEFY----RYLRYKSPKYGPSFRSEYW----FIGV 164 SEYYALPTRDCLFEDPLHNGETMLKIWNLNKFTGV 88

34 35 36 37 38 38
599 590 590 590 590 590 590 590 590 590
10.6 10.6 10.5 10.5
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Q9akq3 Q9akj9 P20409 P16348 P17979 P36433 P50182
rickettsia rickettsia p anthranil solanum tub solanum tub haemophilus neisseria l

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FLA3_PYRKO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.
A Jin-no K., Takahashi M., Sekine M., Babba S.-I., Ankai A., Kosi
A Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
A Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
A Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
A Yamazaki J., Kushida N., Sako Y., Kikuchi H.;
T., Nomura N., Sako Y., Kikuchi H.;
T., Complete genome sequence of an aerobic hyper-thermophilic
T. Crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
C -!- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
C diphosphate + L-glutamyl-tRNA(Glu).
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP000064; BAN
HSSP; P00962; 1GTR
                          Pyrococcus kodakaraensis
Archaea; Euryarchaeota;
                                                                                          16-OCT-2001
16-OCT-2001
                                                                           Flagellin
                                                                                                                                       Q9V2W9;
                                                                                                                                                      FLA3_PYRKO
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aminoacyl-tRNA synthetase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRFAMS; TIGR00463; gltx_arch; 1. PROSITE; PS00178; AA_TRNA_LIGASE_I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00749; tRNA-synt_1c; PRINTS; PR00987; TRNASYNTHGLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99310339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                      16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR004526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aeropyrum pernix.
                                                                                                                                                                                                                                 187
                                                                                                                                                                                                                                                                                          140
                                                                                                                                                                                                                                                            61 TRDCLFEDPLHNGETMLK 78
                                                                                                                                                                                                                                                                                                                     3 WD--MFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                          WDEEYIQSLRMEVFYSVARRAIERGCAYV-DNCGREGKELLS
                                                                                                                                                                                                                                TRDLGPEDNLELFEKMLE
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                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                           ВЗ
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IPR001412; trna-synt_I.
                                                                                                                                                                                                                                                                                                                                                                                                                  544 AA;
                                                                                      (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                          precursor.
                                                                                                                                                      STANDARD;
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62894 MW;
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35.9%;
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                              Thermococci;
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5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      Score 69.5;
Pred. No. 5
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; 52B85CDB3EEAA984 CRC64;
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                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FALSE_NEG
                              Thermococcales; Thermococcaceae;
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                                                                                        update)
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Best Local S
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SCIENCE 281:375-388(1998).
THE MRAZ FAMILY
THE IS
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                                                                                                                                                                                                                                                                                                                                                         Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J. Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garlan Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99413236; PubMed=10483738;
Nagahisa K., Ezaki S., Fujiwara S., Imanaka T., Takagi M.;
Nagahisa K. Ezaki S., Fujiwara S., Imanaka T., Takagi M.;
Sequence and transcriptional studies of five clustered flagellin
genes from hyperthermophilic archaeon Pyrococcus kodakaraensis KO
FEMS Microbiol. Lett. 178:183-190(1999)
                                     the
                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute There are no restrictions on its the Fundamental Control of the Fundament Control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treponema pallidum.
Bacteria; Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB018434; BAA84107.1; InterPro; IPR002774; Arch_flagellin. Pfam; PF01917; Arch_flagellin; 1.
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                                                                                                                                                                                                                                                                                                                                   Venter
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                                                                                                                                                                                                                                                                                          "Complete genome sequence of Treponema pallidum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002
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15-JUN-2002
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                                     European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                   J.C.
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41, Last seq
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Last annotation
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HSSP: P22121; 2HTS.
TRANSFAC; T03449; -.
SGD: S0003908; YJR147W.
INTERPRO; IPRO00232; HSF_DNA_bind.
InterPro; IPR0002341; HSF_ETS.
Pfam: PF00447; HSF_DNA-bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last seq
16-OCT-2001 (Rel. 40, Last ann
Hypothetical 41.2 kDa protein
YJR147W OR J2204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases |- SUBCELLULAR LOCATION: Nuclear (Potential). |- SIMILARITY: BELONGS TO THE HSF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
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TIGRFAMS; TIGR00242; TIGR00242;
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                                                                                                                                                                                                                                                          SMART: SM00415; HSF; 1.

PROSITE: PS00434; HSF_DOMAIN; FALSE_NEG.
Hypothetical protein; Nuclear protein; DNA
Hypothetical protein; BY SIMILARITY
DNA_BIND 12 116 BY SIMILARITY
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an email to license@isb-sib.ch).
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PM17_MOUSE
Q60696;
CARBOHYD
CARBOHYD
CARBOHYD
VARIANT
                                           REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
CARBOHYD
                                                                                                           DOMAIN
DOMAIN
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REPEAT
                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Last annotation update)
Melanocyte protein Pmel 17 precursor (Silver locus
SILV OR PMEL17 OR D10H12S53E OR SI.
                                                                                                                                                                                                                                              Pfam; PF00801; PKD; SMART; SM00089; PKD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6; TISSUE=Skin; MEDLINE=95175358; PubMed=7870580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                         DOMAIN
                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                               Disease mutation
                                                                                                                                                                                                                          Transmembrane;
                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                          EMBL; U14133; AAA69538.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   <del>; ;</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              putative cytoplasmic domain of Pmel Nucleic Acids Res. 23:154-158(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bennett D., Pickard R.T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kwon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                 MGD; MGI:98301;
                                                                                                                                                                                                                                                                   InterPro; IPR000601; PKD_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse silver mutation is caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236
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                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: COULD BE A MELANOGENIC ENZYME.
SUBCELLULAR LOCATION: Type I membrane protein (Potential).
TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN MELANOCYTES.
DISEASE: DEFECTS IN SILV ARE THE CAUSE OF THE SILVER COAT COLOR WHICH SEEMS TO BE DUE TO PREMATURE DEATH OF PIGMENT CELLS DURING
                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE PMEL-17/NMB FAMILY. SIMILARITY: CONTAINS 1 PKD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                             THE HAIR CYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B.S., Halaban R., Ponnazhagan S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELSETP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FHA------YQTANFLQENFEAIKKVVCPDSCLQHQQRQPKRPKRYSLLLLIPNAS 235
                                                                                                                                                                                                                                     PS50093; PKD;
 Z.
                                                                                                                                                                                                                        Glycoprotein;
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S -> L (I
                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                  EXTRACELLULAR POTENTIAL.
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                                                                                                                                                                                         MELANOCYTE PROTEIN PMEL
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Sciurognathi; Muridae;
                                                                                                                                   13
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 (IN SILVER)
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(GLCNAC.
(GLCNAC.
                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim K.
                                                                                                                                  APPROXIMATE TANDEM
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(POTENTIAL).
(POTENTIAL).
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Murinae; Mus
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MBL outstation -
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RESULT 7
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                                                                                                                                                                                                                                                                                 InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                            SEQUENCE
                                                                                                                                                                                                                    Pfam; PF03302; VSP; 1.
SMART; SM00181; EGF; 3
SMART; SM00261; FU; 5.
                                                                                                                                                                                                                                                                                                                                        EMBL; M95814; AAA02687.1;
PIR; A48579; A48579.
HSSP; P02468; 1KLO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Isolate AD-1;
MEDLINE=93241215; Pubmed=8479449;
EY P.L., Khanna K., Manning P.A., Mayrhofer G.;
"A gene encoding a 69-kilodalton major surface
                                                                 CARBOHYD
                                                                                 CARBOHYD
                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Giardia lamblia
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15-JUL-1998
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                                                                                                     DOMAIN
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                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intestinalis trophozoites.";
mol. Biochem. Parasitol. 58:247-258(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLASMA MEMBRANE.

DOMAIN: CONTAINS 27 REPEATS OF A CXXC MOTIF.

SIMILARITY: BELONGS TO THE GIARDIA VARIANT SURFACE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: TYPE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEWTEVQGSNCWRGGQVSLRVINDGPTLVGANASFSIALH-FPGSQK-VLPDGQVIWANN 107
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                                                                                                                                                                                                     Repeat; Transmembrane;
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IPR002174; Furin-like.
IPR005127; Giardia_VSP
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667
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Diplomonadida;
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(Rel. 29, Last sequence up
(Rel. 36, Last annotation
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                                        CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (P
N-LINKED (GLCNAC. . .) (P
, LDD9572703232B8D CRC64;
                                                                                                                      MAJOR SURFACE TROPHOZOITE EXTRACELLULAR (POTENTIAL).
    Score
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Pred. No. 21;
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                                                                                                                                                                                                 Signal.
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(IN SILVER).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
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Length
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                                                                                                                                                            ANTIGEN 11
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Matches 18; Conservative
                                                                                                                                       Query Match
Best Local
                                                                                                                          Matches
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P44819;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Thiosulfate sulfurtransferase glpE (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F. Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M. McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C. Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Septem C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- FUNCTION: Catalyzes, although with low efficiency, the sulfur transfer reaction from thiosulfate to cyanide (By similarity).
-:- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.
-:- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-:- SIMILARITY: BELONGS TO THE GLPE FAMILY.
-:- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rd."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gnehm C.L.
Venter J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
STRAINE=95350630; PubMed=7542800;
                                                                                                                                                                                                                                               Pfam; PF00581; Rhodanese; 1.
                                                                                                                                                                                                                                                                               HSSP; P09390;
TIGR; HI0679;
                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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NCBI_TaxID=727;
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                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                    Transferase; Glycerol metabolism; Complete proteome ACT_SITE 63 63 BY SIMILARITY.
                                                                                                                                                                                                                                    SMART;
                                                                                                                                                                                                                                                                                                               EMBL; U32750;
                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus influenzae
                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                        Local Similarity
 56
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 DSPIIVSCYHGVSSR---
                                DGSILRSEYYALPTRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR
                                                             WEMMQQGAILVDIRDNMRFAYSHPKGAFHLTNQ
                                                                                                                                                                                                                                    SM00450; RHOD;
                                                                                                                                                                                                                                                                  IPR001763; Rhodanese-like
                                                                                                                                                                                     105 AA;
                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                               AAC22338.1;
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                                                                                                                                                                                       12033 MW;
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                                                                                           THPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gamma subdivision; Pasteurellaceae;
                                                                                                                          13;
                                                                                                                                       Score 64;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
NVATFLVEQGYKNVFSMIGGFD---
                                                                                                                                                                                     A3120E14BDD7245F CRC64;
                                                                                                                          Mismatches
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RESULT 9

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Best Local S
Matches 28
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STRAIN-Sprague-Dawley;
MEDLINE-21181710; PubMed-11285252;
Nishimura D.Y., Searby C.C., Carmi
                                                                                                                                                      15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Bardet-Biedl syndrome 2 protein homolog.
                                                                                                                                                                                                                    Q99мн9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nonstructural protein; RNA-binding. DOMAIN 384 400 DRBM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porcine rotavirus (group C / strain Cowden).
Viruses; dsRNA viruses; Reoviridae; Rotavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1992 (Rel. 23, 
01-AUG-1992 (Rel. 23, 
15-JUL-1998 (Rel. 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VN34_ROTPC
                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                  BBS2_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nonstructural RNA-binding protein 34 (NS34) (NCVP4).
                                                                                                                         Rattus norvegicus (Rat)
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                                                 SEQUENCE FROM N.A.
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InterPro; IPR001159; DS_RBD.
InterPro; IPR002873; Rota_NSP3.
                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yfam; PF00035; dsrm; 1.
Yfam; PF01665; Rota_NSP3; 1.
PROSITE; PS50137; DS_RBD; 1.
                                                                                                                                                                                                                                                                                                           258 NESPD--FD--VWNERSNLKIVSIND-CHAICVFKFENAWWC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              402 AA;
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                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45125 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                              11.3%; Score 63.5;
27.5%; Pred. No. 16
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010336;
01-NOV-1997
                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polyhedrosis virus genome.";
Virology 229:381-399(1997),
-i- SIMILARITY: TO CORRESPONDING ORF IN ACMNPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation of the control of 
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Hum. Mol. Genet. 10:865-874(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stone E.M., Sheffield V.C., "Positional cloning of a novel gene on
                                                                                                                                                 InterPro; IPR002557; Chitin_bind_PerA. Pfam; PF01607; CBM_14; 2. SMART; SM00494; ChtBD2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-97271300; PubMed-9126251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Orgyła pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF342738; AAK28554.1; -. SEQUENCE 721 AA; 79917 MW;
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                                                                                                                                                                                                                                  EMBL; U75930; AAC59085.1; -
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"The sequence of the Orgyia |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=164623;
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                                                                                                   al protein.
819 AA; 9
  Conservative
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Kwitek-Black A.E., Ying L., Duhl D.M.,
naccone A., Bonneau D., Biesecker L.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                        91067 MW;
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Last annotation update)
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Pred. No. 32;
L9; Mismatches
                             Pred. No.
                                                Score 63.5;
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                             36;
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                                                   DB 1;
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                                                                                                                                                                                                                                                                                                          http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                Usage
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                                                Length 819;
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Gorman S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jacobson S
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10;

Mismatches

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                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sentitles.com/server/memodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (2)
CHARACTERIZATION.
MEDLINE-97274210; PubMed-9110970;
MEDLINE-97274210; PubMed-9110970;
MEDLINE-97274210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge Benes V. Bruckner M., Delius H., Dubois E., Dusterboft A., Entian K.D., Floeth M., Goffeau A., Hebling U., Heumann K., Entian K.D., Floeth M., Goffeau A., Hebling U., Heumann K., Heuss-Weitzel D., Hilbert H., Hilger F., Kleine K., Kotter P., Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Mostl D., Mueller Auer S., Nentwich U., Obermaier B., Piravandl E., Pohl T.M. Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S., Underwood A.P., Urrestarau L.A., Vandenbol M., Verhasselt P., Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=S288c / AB972;
MEDLINE=97313267; PubMed=9169871;
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16-OCT-2001
                               InterPro; IPR000477; RVTse.
InterPro; IPR003545; Telomerase_RT
                                                                                          EMBL; U20618; AAB64520.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          telomerase."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 387:87-90(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                     ence 276:561-567(1997).
FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR THE REPLICATION OF CHROMOSOME TERMINI IN MOST BUKARYOTES. IT ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.
SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: DELETION CAUSES TELOMERE SHORTENING AND SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY
                                                                                                                                                                                                                                                                                    TELOMERASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OR YLR318W OR L8543.12
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                                                                                                                             equires a license agreement (femail to license@isb-sib.ch)
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(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
reverse transcriptase (EC 2.7.7.-)
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                 rvt;
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RESULT 13
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Best Local
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P08619;
01-AUG-1988
01-MAY-1992
01-NOV-1995
                                                                                                                                                                       MEDLINE-900000...
Okamoto P.M., Marzluf G.A.;
"Nitrate reductase of Neurospora crassa: the "Nitrate reductase of in the heme domain as
                                                                                                                                                                                                                                                                                           Okamoto P.M., Garrett R.H., Marzluf G.A.; "Molecular characterization of conventional and new repeat-induced mutants of nit-3, the structural gene that encodes nitrate reductas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase; RNA-directed DNA polymerase; Telomere; Nuclear DNA-binding.
SEQUENCE 884 AA; 102663 MW; 788334BB49592340 CRC64;
                                                                                                                                                               site-directed mutagenesis
                                                                                                                                                                                                                                                                                                                                    STRAIN=74-OR23-1A;
MEDLINE=93241176; PubMed=8479443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        crassa: nucleotide sequence and regulation of mRNA synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Okamoto P.M., Fu Y.-H., Marzluf G.A.; "Nit-3, the structural gene of nitrate reductase in Neurospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=74-OR23-1A;
                                                                                                                                                                                                                         MEDLINE=93360901;
                                                                                                                                                                                                                                        MUTAGENESIS
                                                                                                                                                                                                                                                               in Neurospora crassa.";
Mol. Gen. Genet. 238:81-90(1993).
                                                                                                                                                                                                                                                                                                                                                                  MUTANTS
                                                                                                                                                                                                                                                                                                                                                                                           in Neurospora crassa assimilatory nitrate reductase.";
EMBO J. 2:1909-1914(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91287699; PubMed=1829499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nitrate reductase
                                                                                                                                                                                                                                                                                                                                                                                                                      "On the presence of a heme-binding domain homologous to cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                     Lе К.Н.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY PARTIAL
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       STEP OF NITRATE ASSIMILATION IN PLANTS, FUNGI AND BACTERIA.

CATALYTIC ACTIVITY: NADPH + nitrate = NADP(+) + nitrite + H(2)0.

COFACTOR: EACH SUBUNIT CONTAINS 1 EQUIVALENT OF FAD, HEME IRON,

AND MOLYBDENUM-PERIN AS PROSTHETIC GROUPS. THE HEME GROUP IS

CALLED CYTOCHROME B-557.

PATHRAY: NITRATE ASSIMILATORY PATHWAY.

SUBUNIT: HOMODIMER.

INDUCTION: ITS EXPRESSION IS HIGHLY REGULATED AND RESPONDS RAPID

TO NITRATE INDUCTION AND TO NITROGEN REPRESSION.
                                                                                                                                       . Gen. Genet. 240:221-230(1993). FUNCTION: NITRATE REDUCTASE IS A KEY ENZYME INVOLVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MLKIWNLNKFTGVIGAFN 93
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23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genet. 227:213-223(1991)
                                                                                                                                                                    amino acids in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sordariaceae;
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                                                                                                                                                                                                                         PubMed=8355655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08, Created)
22, Last sequence update)
32, Last annotation update)
[NADPH] (EC 1.6.6.3) (NR).
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EUKARYOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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29.5%;
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Pred. No.
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 MOLYBDOPTERIN
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                                                                                                                                                                               functional role examined by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sordariomycetes;
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Best Local S
Matches 31
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Pfam: PF00174; oxidored_molyb; 1.
Pfam: PF00175; NAD_binding; 1.
Pfam: PF00175; NAD_binding; 1.
Pfam: PF00970; FAD_binding; 6; 1.
Pfam: PF00970; FAD_binding; 6; 1.
Pfam: PF00970; FAD_binding; 1.
Pfam: PF00970; FAD_binding; 1.
PFRNTS; PR00406; CYTDSRDTASE.
PRINTS; PR00407; EUMOPTERIN.
PRINTS; PR001612; CYTDCHROME_B5.
PROSITE; PS00151; CYTDCHROME_B5_1; 1.
PROSITE; PS00159; MOLYBDOPTERIN_EUK; 1.
PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
    30-MAY-2000
30-MAY-2000
16-OCT-2001
                                                                         Y872_RICPR
Q9ZC94;
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MUTAGEN
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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BINDING
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001199; Cyt_B5.
InterPro; IPR001334; Cyt_B5_reductase.
InterPro; IPR00572; Euk_Mb_oxred.
InterPro; IPR005066; Mo-co_dimer.
InterPro; IPR001433; Oxred_FAD/NAD(P).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; x61303; CAA43600.1; -. PIR; S16292; S16292. PIR; S34796; S34796. PIR; S37298; S37298.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 PDWDMFQ--STHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 1 CYTOCHRO SIMILARITY: TO FAD/NAD-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C-TERMINAL DOMAIN
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                                                                                                                                                                                                                    QGRGVC
                                                                                                                                                                                                                                                             OCCCMC
                                                                                                                                                                                                                                                                                                            SDGTLERGTLRVLVKIYYASPTED-----IKGGQMTQALDALALGKAVEFKGPVGKFVY 835
                                                                                                                                                                                                                                                                                                                                                     -----TMLKIWNLNKFTGVIGAFNC 94
                                                                                                                                                                                                                                                                                                                                                                                                      PDTKIFHFALSHPAQSI------GLP-----VGQHLMMRLPDPAKPTESIIRAYTPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
(Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                    841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               982 AA;
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                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred.
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MOLYBDENUM-PTERIN (POTENTIAL).
INTERCHAIN (POTENTIAL).
INTERCHAIN (POTENTIAL).
HEME-BINDING (BY SIMILARITY).
HEME LIGAND (BY SIMILARITY).
HEME LIGAND (BY SIMILARITY).
HEME LIGAND (BY SIMILARITY).
HEME LIGAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H->A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NADP (BY SIMILARITY).
H->A: LITTLE LOSS OF ENZYME ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAD;
                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B7838C031B19687F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NADP; Heme; Molybdenum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO.
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51;
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L outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                 API2_SOLTU STANDARD: PRT: 220 AA. 043646; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Aspartic protease inhibitor 2 precursor (Catholinh) (Cathlin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund Eriksson A.-S., Winkler H.H., Kurland C.G.,
                                                                                                                                   Solanum tuberosum L.";
Plant Mol. Biol. 26:73-83(1994)
                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-CV. AM 80.5793; TISSUE-Leaf;
MEDLINE-95036033; PubMed-7948907;
Herbers K., Prat S., Willmitzer L.;
                                                                                                                                                                                                                                                                     Solanum tuberosum (Potato).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
Asteridae; euasterids I; Solanales; Solanacea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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MEDLINE=99039499; PubMed=9823893;
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Rickettsiaceae; Rickettsieae; Rickettsia.
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                                                                                                                        Plant Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ235273; CAA15296.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rickettsia
                                                                                                                                                                                                                                                          NCBI_TaxID=4113;
                                                                                                                                                               "Cloning and characterization of a cathepsin D inhibitor gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The genome sequence of Rickettsia prowazekii and
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WOUNDING.
SIMILARITY:
FAMILY.
                                                        FUNCTION: INHIBITOR OF CATHEPSIN D (ASPARTIC PROTEASE). MAY ALSO INHIBIT TRYPSIN AND CHYMOTRYPSIN (SERINE PROTEASES). PROTECTS THE PLANT BY INHIBITING PROTEASES OF INVADING ORGANISMS. SUBCELLULAR LOCATION: Vacuolar (By similarity). TISSUE SPECIFICITY: TUBERS.
                                          INDUCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -NKFTGQENKIDC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al protein;
165 AA; 19
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              BELONGS
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31.5%;
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9411 MW; 305290A3A14024C4 CRC64;
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              THE LEGUMINOUS KUNITZ-TYPE
                                          BY ABSCISIC ACID, JASMONIC ACID AND
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Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                  precursor (Cathepsin
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                                                                                                                                                                                                                                                                           Solanaceae;
                                                                                                                                                                                                                                                                                                   Embryophyta;
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eudicots;
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               INHIBITOR
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in no way
commercial
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Search completed: March 27, 2003, 10:04:21 Job time: 19.628 secs
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Best Local Similarity
Matches 25; Conserv
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CARBOHYD
SEQUENCE
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CHAIN
SITE
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                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                            ACT_SITE
                                                                                                                                                                                                                                                                                                      ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                               ProDom: PD000891; Kunitz_legume; 1.
SMART; SM00452; STI; 1.
PROSITE: PS00283; SOYBEAN_KUNITZ; 1
Aspartic protease inhibitor; Serine
Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00197; Kunitz_legume; PRINTS; PR00291; KUNITZINHBTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X74985; CAA52919.1; -
                                                InterPro; IPR002160; Kunitz_legume.
                                                                                                       49
                                                                                                                          10 HPCAAFHAAS--RAISGGPIYVS------DSVGKHNFDLLKKLVLPDGSILRSEYY 57
                                                                                                      NPNSSYRIISIGRGALGGDVYLGKSPNSDGPCPDGVFRYNSD-----VGPSGTFVR---- 99
                                                                                                                                                                                                            220 AA;
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174
51
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inhibitor; Serine protease inhibitor; Signal;
                                                                                                                                                                                                            125 B
185 B
51 N
24199 MW;
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32
220
31
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                                                                                                                                                                    11.1%; Score 62.5;
25.0%; Pred. No. 11;
                                                                                                                                                         15;
                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCWAC. . .) (POTENTIAL).
33D6E866EA0C5DD5 CRC64;
                                                                                                                                                                                                                                                              REACTIVE BOND (FOR TRYPSIN) (BY SIMILARITY).

REACTIVE BOND (FOR CHYMOTRYPSIN) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                  SIMILARITY)
                                                                                                                                                                                                                                                                                                                             ASPARTIC PROTEASE INHIBITOR 2. VACUOLAR TARGETING SIGNAL (BY
                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                       Mismatches
                                                                                                                                                                                DB 1;
                                                                                                                                                       27;
                                                                                                                                                                               Length 220;
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Minimum DB
Maximum DB
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and is derived by analysis of
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Listing first 45 summaries
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/cgn2_6/ptodata/1/laa/FCTUS_COMB.pep:*
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PCT-US93-04392-3
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US-09-193-510-5
US-09-368-402-5
US-09-325-932A-179
US-09-325-932A-648-10
PCT-US93-04392-6
PCT-US93-04392-12
PCT-US93-04392-12
PCT-US93-04392-15
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US-08-948-616-10
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US-08-851-843A-55
US-08-974-549A-222
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10.1	10.1	10.1	10.1	10.1	10.1	10.2	10.2	10.2	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.3
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Sequence 29, Appl	Sequence 22, Appl	Sequence 24, Appl	Sequence 114, App	Sequence 114, App	Seguence 114, App	Sequence 2, Appli		1	Sequence 6, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 8, Appli	Sequence 11, Appl	Sequence 55, Appl

ALIGNMENTS

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US-08-846-234-5
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                                                                                                                  Matches 101;
                                                                                                                                                   Query Match
                                                                                                                                     Best
                                                                                                                                                                                                                                 TELEFAX: (703)-413-2220
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 784 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703).413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PRODUCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: OBLON
STREET: 1755 S.
CITY: ARLINGTON
STATE: VIRGINIA
                                                  510
                 61
                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                  1 PDWDMEQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60
                   TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR 101
                                                  PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP
h 100.0%;
Similarity 100.0%;
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                                                                                                                                                                                                                      linear
                                                                                                                                                                                                   protein
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                                                                                                                  0;
                                                                                                                  Score 564; DB 4;
Pred. No. 1.2e-64;
Mismatches 0;
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                                                                                                                                                Length 784;
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US-09-153-586-23
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SEQ ID NO 23
LENGTH: 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 55,
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23, Application US/09153586A Patent No. 6270772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 48823
CURRENT APPLICATION N
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TITLE OF INVENTION: Recombinant MHC molecules useful for manipulation
TITLE OF INVENTION: antigen-specific T-Cells
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                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                        APPLICANT: Andrews, William H.
TITLE OF INVENTION: NO. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
         PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/846,017
                                                                                                    CURRENT APPLICATION DATA:
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                                                                     APPLICATION NUMBER: FILING DATE: 06-MA
                                                                                                                                                                                                                    ZIP:
                                                                                                                                                                                                                                   COUNTRY:
                                                  CLASSIFICATION:
                                                                                                                     SOFTWARE:
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                                                                                                                                                                                                                                                                       San Francisco
                                                                                                                                                                                                                                  California
United States of America
                                                                                                                                                                                                                                                                                        E: Townsend and Townsend and Crew LLP Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                              Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
                                                                                                                       PatentIn
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                                                                   UMBER: US/08/851,843A
06-MAY-1997
25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thomas R
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26.2%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                              FILING DATE: 01-OCT-PRIOR APPLICATION DATA:
                                                       PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/724,643
                                                                                                                                                SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                                  FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                STREET: Two Embarcac
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 MLKIWNLNKFTGVIGAFN 93
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REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    884 amino acids
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Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lingner, Joachim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (415) 576-0300
                                                                                                                                                                PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                  Townsend and Townsend and Crew LLP Townsend and Townsend and Crew LLP
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18-APR-1997
                                                 01-OCT-1996
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29.5%;
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                 US 08/844,419
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Pred. No.
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24;
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                                                                                                                                                           Sequence 55, Applicate Patent No. 6261836 GENERAL INFORMATION:
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                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT: Harley, Caryin APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase NUMBER OF SEQUENCES: 225
                                                                                  APPLICANT:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Protein LOCATION: 1.884 OTHER INFORMATION: OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 23; Conservative
                                                                                                                                                                                               Application US/08854050
                                                                  Morin, Gregg B.
Harley, Calvin
                                                                                                  Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                 Cech, Thomas R.
                                                                                                                                Lingner, Joachim
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09-MAY-1997
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01-OCT-1997
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14-AUG-1997
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ESTp (L8543.12)"
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RESULT 6
US-09-430-323-55
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Best Local S
                                                                                                                             Sequence 55, Application US/09430323 Patent No. 6309867 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           Matches
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: not rele
MOLECULE TYPE: pept.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
FILING DATE: 01-OCT-1996
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APPLICATION NUMBER:
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APPLICATION NUMBER:
FILING DATE: 25-APR-
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PRIOR APPLICATION DATA:
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SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01
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CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 23; Conserv
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   TITLE
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     OF.
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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E: peptide
   Andrews, INVENTION:
                                 Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
                                                                                                                Cech,
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                                                                             Nakamura, Toru
                                                                                             Lingner, Joachim
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William H.
No. 6309867el Telomerase
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Pred. No. 24;
15; Mismatches
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; MOLECULE TYPE: peptide ; SEQUENCE DESCRIPTION: SEQ ID NO: 55: US-09-430-323-55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
        APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNI
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
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STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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TELEPHONE: (415) 576-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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LENGTH: 884 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                       PTQIADRIKEFKQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKDALKNENGFF 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: not relevant TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/430,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: California
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                                                                                                                                                                              DeHoff, Bradley S.
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                                                                              POLYKETIDE SYNTHASE GENES: 15
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29.5%;
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Pred. No.
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US-08-804-227C-4
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: x-83
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acid
                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 15,
FILING DATE: MAY 15,
                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04392
TOPOLOGIE TYPE: CDN
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2602 TTDP-AAFYAEFAERGYDYGPAFQGFTAGARHGEDVVAEVALPSGLVADARHHRL 2655
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LENGTH: 3729 amino acids
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                                   STRANDEDNESS: doub
TOPOLOGY: circular
                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: ASCI(DOS) Text
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                                                                          AMINO ACID
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                                                                                       430 amino acids
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VENTION: Enzymatic Process for Production
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Pred. No.
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                                                               US-08-948-616-5
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Best Local S
Matches 25
Best Local
Matches 1
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                              Query Match
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                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN: 511
INDIVIDUAL ISOLATE:
IMMEDIATE SOURCE:
CLONE: ZL511 1-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: VESICLE TRANSPORT ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                      TELEPHONE: 650-855-0555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hillman, Jennifer L.
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nes 25; Conserv
                                                                            LIBRARY: KERANOT02
CLONE: 2620104
                                                                                                                           TOPOLOGY: 11
                                                                                                                                                         LENGTH: 210 aminc TYPE: amino acid
                                                                                                                                                                                                                                                                                      NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: Herew
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l Similarity 33.3
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Shah, Purvi
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DN: 530
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25.5%; Pred. No. 18;
           10.6%;
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 10; Mismatches
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             Score 60; DB 2;
Pred. No. 7.8;
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US-09-193-510-5
                                  RESULT 11
US-09-368-402-5
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Best Local Similarity 33.3
Conservative
Sequence 5, Application US/09368402 Patent No. 6200790
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                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEPAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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APPLICANT: Shah, Purvi
APPLICANT: COrley, Neil C.
TITLE OF INVENTION: VESICLE TRANSPORT ASSOCIATED PROTEINS
                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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CITY: Palo Alto
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CLONE: 2620104
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TOPOLOGY: lir
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                                                                                                   60 VKGKPVHLHIWDTAGQDDYDRLRPLFYPDASVL 92
                                                                                                                                22 ISGGPI--YVSDSVGKHNFDLLKKLVLPDGSIL 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94304
                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                 210 amino acids
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                                                                                                                                                                                                                                                                    KERANOT02
                                                                                                                                                                                                                                                                                                  SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diskette
                                                                                                                                                                                 10.6%; Score 60; DB 2; 33.3%; Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08/948,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36,749
                                                                                                                                                                    10;
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                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                   Length 210
                                                                                                                                                                    Indels
                                                                                                                                                                  2
                                                                                                                                                                    Gaps
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GENERAL INFORMATION:
APPLICANT: Hillma
APPLICANT: Lal, P

Hillman, Jennifer L.

1:

Lal, Preeti

APPLICANT: APPLICANT:

Corley, Neil C. Shah, Purvi

TITLE OF INVENTION: NUMBER OF SEQUENCES:

VESICLE TRANSPORT ASSOCIATED PROTEINS: 11

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CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILLING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 179
LENGTH: 608
TYPE: PRT
ORGANISM: Pinus radiata
                                                                US-09-325-932A-179
                                                                                                                                                                                                                                                                                                                                          US-09-325-932A-179
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                                                                                                                                                                                                                                                                                                             Sequence 179, Application US/09325932A Patent No. 6451604
                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Flinn, Barry
                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
 Matches
                 Best Local Similarity
                                                                                                                                                                                                                 APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting
TITLE OF INVENTION: death and their use in
FILE REFERENCE: 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 33.1 hes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                60 VKGKPVHLHIWDTAGQDDYDRLRPLFYPDASVL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                 22 ISGGPI--YVSDSVGKHNFDLLKKLVLPDGSIL 52 : | |: :: |: |: |: | | | | |: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 3174 Por CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Billings, Lucy J. REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 amino acids
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.6%;
               10.6%; Score 60; 21.4%; Pred. No.
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18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 60; DB 4; Pred. No. 7.8;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                DB 4;
                                                                                                                                                                                                                           programmed cell
the modification of forestry plant devel
48;
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                            Length 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 210;
Indels
26;
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Gaps
5
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CURRENT APPLICATION NUMBER: US/09/342,648
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: 60/092,659
EARLIER FILING DATE: July 13, 1998
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Microsoft Office 97
SEQ ID NO 10
LENGTH: 890
TYPE: PRT
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US-09-342-648-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Freedman, Richard, Heefner, Donald L. APPLICANT: Phelphs, Trish, Roberts, Christopher R. APPLICANT: Salazar, Felix H., Snyder, Roger C. TITLE OF INVENTION: Enzymatic Process for Production NUMBER OF SEQUENCES: 15
                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Beck, Steven R., Cain, Robert O.,
                                                                                                                                                                                                                                                                                   STREET:
CITY:
STATE:
                                                                                                                                                                                                                                           ZIP:
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APPLICATION NUMBER: UPILING DATE: MAY 15,
                                                             CLASSIFICATION:
                                                                             FILING DATE:
                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 TGVIGAFNCOGGGWCR 101
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                                                                               19930514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.6%;
25.0%;
                       us/07/883,658
                                                                                                  PCT/US93/04392
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -CLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQ 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SRAISGGPIYVSDSVGKHNFDLLK-KLVLPD 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                            Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59;
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PRIOR APPLICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/883,65

FILING DATE: MAY 15, 1992

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 430 amino acids

TYPE: AMINO ACID

STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: CDNA
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Zopfiella latipes
STRAIN: 780
INDIVIDUAL ISOLATE: ATCC #44575
IMMEDIATE SOURCE:
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SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: AMINO ACID
STRANDEDNESS: double
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL OFF...
ORGANISM: ZOFF...
ORGANISM: 780
STRAIN: 780
INDIVIDUAL ISOLATE: F
IMMEDIATE SOURCE:
CLONE: 21780-3A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS: ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Beck, Steven R., Cain, Robert O., Chan, Hardy W. APPLICANT: Freedman, Richard, Heefner, Donald L. APPLICANT: Phelphs, Trish, Roberts, Christopher R. APPLICANT: Salazar, Felix H., Snyder, Roger C. TITLE OF INVENTION: Enzymatic Process for Production of NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308 L----MFEDHLTGG---AKKGHEDALNGPVGSF 333
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CITY:
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 19930! CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 LPTRDCLFEDPLHNGETMLKIWNLNKFTGVIGAF 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zopfiella latipes
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PCT-US93-04392-9
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                                                            308 L-----MFEDHLTGG---AKKGHEDALNGPVGSF 333
                                                                                                                                         248 HPDDPLATGKQVLAGGGNMNLVADGDFGGHGMFTTGENYLKVLKSLLANDGKLLSPEMVN 307
                                                                                                                                                              10 HPCAAFHAASRAISGG--PIYVSD------SVGKHNFDLLKKLVLPDGSILRSEYYA 58
                                                                                                 59 LPTRDCLFEDPLHNGETMLKIWNLNKFTGVIGAF 92
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z1780-m10
2003, 10:07:36
                                                                                                                                                                                                                        15; Mismatches
                                                                                                                                                                                                                                                           DB 5; Length 430;
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Search completed: March 27, Job time: 25.6341 secs

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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                             Score
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1: /SIDS2/gcgdata/g
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Match
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Gapop 10.0 , Gapext 0.5
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      IJ
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AAW57818
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ABB93664
AAY32075
AAW32075
AAW32076
AAW32076
AAW320142
                                                                                                                                                                                                                                                                                                            SUMMARIES
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188.389 Million cell updates/sec
Cucumber raffinose Japanese artichoke Amino acid sequenc Herbicidally activ Rapeseed raffinose Mustard raffinose Broad bean raffino Amino acid sequenc Soybean protein: S
                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                Cucumber raffinose
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Mouse melanoma ant	AAY31978	20	625		ū.	
s pol	757	23	423	1.	ū.	
	9	18	207		63.5	
dally acti	373	23	359			
cidally	0	23	336	۲.	65.5	
prote	9	22	2099	٢	67	
prote	AAM79480	22	1778	11.9	67	
l human	721	22	466		m	
human	0942	22	466	2	68.5	
ō	360	22	183	2	m	
Human protein seq		22	615	2	69	
Novel human secre		22	615	۲.	69	
C glutamicum		22	426		69	
H. pylori c	AAW20443	18	412		69.5	
Drosophila melan	ABB64380	22	638		71	
Arabidopsis thal	AAG28629	21	193		79	
Soybean raffing	AAY17421	20	15	4	79	
Peptide Seq ID No	AAY06803	20	174	Ģ	85	
Arabidopsis thali	2	21	229	δ.	205	
Herbicidally act	9	23	807	<u>ب</u>	371	
Wheat raffinose	AAY70981	21	841	8	384	
Rice raf	7	21	770	8	387	
Soybean raffinos		20	750	8	387	
Corn raffinose s	7097	21	508	9	394	
Rice raffinose s	AAY70977	21	763	0.	400	
Corn raffinose sy	7	21	756	1	403	
Wheat raffi	7	21	751	1.	404	
Amino acid sequen	AAY30145	20	271	5	426	
Corn raffinose s	AAW57889	19	271	5	426	
ra	3207	20	265	8	444	
eet raffin	207	20	783		476	
raffinos	7097	21	758	.7	494	
an raffinose	B4940	22	781	8	497	
no acid seque	301	20	781	88.1	497	
Soybean raffinose	AAW57887	19	781	8	497	

ALIGNMENTS

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RESULT 1
AAW53570
PT PT PT PXX
                                                                                                                                      Claim 3; Pages 17-20; 26pp; Japanese
                        Raffinose synthase gene - useful for preparation of raffinose in transformed plant
                                                    WPI; 1998-264858/24.
N-PSDB; AAV22250.
                                                                                                                                                              JP10084973-A.
                                                                                                                                                                                Cucumis sativus
                                                                                                                                                                                                 Cucumber; raffinose synthase; sucrose;
                                                                                                                                                                                                                  Cucumber raffinose synthase.
                                                                                                                                                                                                                                      06-JUL-1998
                                                                                                                                                                                                                                                        AAW53570;
                                                                                                                                                                                                                                                                          AAW53570 standard; Protein; 784 AA
                                                                                                26-JUL-1996;
26-APR-1996;
                                                                                                                            28-APR-1997;
                                                                                                                                              07-APR-1998
                                                                             (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                                      (first entry)
                                                                                                96JP-0198079
96JP-0107682
                                                                                                                            97JP-0111124
                                                                                                                                                                                                 galactinol
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RESULT 2
AAY17417
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is cucumber raffinose synthase, which forms raffinose from sucrose and galactinol, has an optimum pH of 6 to 8 and working temperature of 35 to 40 degrees C, has a molecular weight of 75 to 95 kDa by gel filtration or 90 to 100 kDa by PAGE and SDS-PAGE under reductive conditions and is inhibited by
                                                                                                                                                                          The present invention describes a raffinose synthase, having an activity of forming raffinose from sucrose and galactinol. The raffinose synthase gene can be used for expression in a plant for the production of raffinose. The raffinose synthase can give raffinose from sucrose and galactinol efficiently. The present sequence represents raffinose
                                                                                                                                         Sequence
                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                               New raffinose synthase gene - sucrose and galactinol
                                                                                                                                                                                                                                                                                                                      WPI; 1999-340516/29.
N-PSDB; AAX61238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cucumber raffinose
                                                                                                                                                                  synthase from cucumber.
                                                                                                                                                                                                                                                                                                                                                                                    24-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                            24-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                     11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cucumis sativus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY17417 standard; Protein; 784 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUL-1999 (first entry)
                                      510
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             61
                                                                                                   Local Similarity
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                                                1 PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR 101
                                   PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 569
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Similarity
                                                                                                                                                                                                                                                     Page 25-27; 37pp; Japanese.
                                                                                                                                         784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   784 AA;
                                                                                       Conservative
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                                                                                    Score 564; DB 20; Pred. No. 3.3e-63; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 564
Pred. No.
                                                                                                                                                                                                                                                                                             for production of raffinose from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 564; µp _
No 3.3e-63;
0:
                                                                                                               Length
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is the Japanese artichoke raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides are useful as organism or cell is changed. Raffinose oligosaccharides are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
                                                                                                                                                                             AAY30144 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   food additives with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SUMO ) SUMITOMO CHEM CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     401
                                                                                                                                                                                                                                                                                                                               461 TRDCLFEDPLHNGKTMLKIWNYNKFTGVVGTFNCQGGGWSR 501
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                                                                                                                                                                                                                                                                                                                                                              TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96JP-0338673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97EP-0122417.
                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      beneficial effects on the gastrointestinal flora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.3%;
89.1%;
                                                                                                                                                                             587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    587 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
                                                                                                                                                                             AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    515; DB 19;
No. 4.4e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bу
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Amino acid sequence of a raffinose synthase protein.

26-OCT-1999

(first

entry)

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ABB93664
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a raffinose synthase protein. The sequence is isolated from plant material. The protein forms raffinose by complexing alpha(1 to 6). D-galactosyl hydroxyl group of the 6C of D-glucose residue in sucrose molecules.
Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 30-31; 40pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ10003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-NOV-1997;
18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP11215984-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stachys sieboldii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Raffinose synthase;
                                                                                                                             07-FEB-2002
                                                                                                                                                WO200210210-A2
                                                                                                                                                                                                                           31-MAY-2002
                                                                                                                                                                                                                                             ABB93664;
                                                                                                                                                                                                                                                               ABB93664 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New raffinose synthase gene - is prepared from a plant material
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-AUG-1999
                              WPI; 2002-269010/31.
                                                Tietjen K,
                                                                                                                                                                 Arabidopsis thaliana.
                                                                                                                                                                                    Herbicidal;
                                                                                                                                                                                                      Herbicidally active polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-DEC-1997;
                                                                  (FARB ) BAYER AG
                                                                                      28-AUG-2001; 2001WO-EP09892
                                                                                                         28-AUG-2001; 2001WO-EP09892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                               461 TRDCLFEDPLHNGKTMLKIWNYNKFTGVVGTFNCQGGGWSR 501
                                                                                                                                                                                                                                                                                                                                                     401
                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                  1999-511112/43.
                                                                                                                                                                                                                                                                                                                          TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR 101
                                                                                                                                                                                                                                                                                                                                                                                          90;
                                                                                                                                                                                                                                                                                                                                                                                                                                 587 AA;
                                                Weidler
                                                                                                                                                                                    plant; agriculture;
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97JP-0329006.
96JP-0338673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97JP-0342899
                                                 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plant; sucrose; raffinose.
                                                                                                                                                                                                                                                                                                                                                                                                   91.3%;
89.1%;
                                                                                                                                                                                                                                                                 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Japanese.
                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                 Score 515; DB 20;
Pred. No. 4.4e-57;
                                                                                                                                                                                                                                                                ξ
                                                                                                                                                                                     herbicide
                                                                                                                                                                                                       SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         6;
                                                                                                                                                                                                                                                                                                                                                                                                          Length 587;
                                                                                                                                                                                                                                                                                                                                                                                         Indels
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RESULT 6
AAY32075
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XX
PF
Qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local Similarity
                                                                           30-APR-1998;
30-APR-1998;
04-DEC-1998;
10-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding the are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising alighing and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from plant with nucleic acid or amino acid sequences from non-plant organisms - \,
N-PSDB; AAZ20210
                                                                                                                                                                                                               Misc-difference 148
                                                                                                                                                                                                                          /note=
Misc-difference 144
                                                                                                                                                                                                                                                 /note-
Misc-difference 143
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
Misc-difference 129
                                                                                                                                                                                                                                                                                                                                        Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                          17-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                               AAY32075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY32075 standard;
          WPI; 1999-593144/51
                                                                                                                                   27-APR-1999;
                                                                                                                                                        03-NOV-1999
                                                                                                                                                                                                                                                                               Misc-difference 132
                                                                                                                                                                                                                                                                                                                                                            Raffinose synthase; rapeseed; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                   Rapeseed raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful as herbicides.
                               Watanabe E,
                                                                                                                                                                               EP953643-A2
                                                    (SUMO ) SUMITOMO CHEM CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRDRLFEDPLHDGKTMLKIWNLNKYTGVIGAFNCQGGGWCR 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDWDMFQSTHPCAEFHAASRAISGGPIYISDCVGKHDFDLLKRLVLPNGSILRCEYYALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               783 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                Oeda K;
                                                                                                 98JP-0120550
98JP-0120551
                                                                           98JP-0345590
98JP-0351246
                                                                                                                                  99EP-0107430
                                                                                                                                                                                                     /note-
                                                                                                                                                                                                                                                                                           /note= "encoded by
                                                                                                                                                                                                                                                                                                                                                                                   synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.6%;
                                                                                                                                                                                                                                               "encoded
                                                                                                                                                                                                   "encoded by CGR'
                                                                                                                                                                                                                         "encoded
                                                                                                                                                                                                                                                                     "encoded by GGW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 511; DB
Pred. No. 2.2e
7; Mismatches
                                                                                                                                                                                                                         γď
                                                                                                                                                                                                                                               by ccs"
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                                                                                                                                                                                                                                                                                            GGY"
                                                                                                                                                                                                                           TCR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ۵.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
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RESULT 7
AAY32074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents rapessed raffinose synthase, a protein that can bind a D-galactosyl group through an alpha(1-6) bond to the hydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. cDNA (see AAZ20210) encoding the enzyme was isolated from rapessed cy. Westar leaf cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see AAZ20207-10) may be used to obtain other raffinose synthase genes by labeled detection or amplification cother raffinose synthase genes by labeled detection or amplification (claimed). These genes may be used to control the levels of raffinose produced in plants. Antisense genes to increase the level of gene activity. The resulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, or providing general health advantages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                         30-APR-1998;
30-APR-1998;
04-DEC-1998;
10-DEC-1998;
     New
                                       N-PSDB; AAZ20209
                                                                                                Watanabe
                                                                                                                                                                                                                                                                                                              03-NOV-1999
                                                                                                                                                                                                                                                                                                                                                 EP953643-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brassica juncea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mustard raffinose synthase.
                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY32074 standard; Protein; 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New sense and antisense genes, useful for altering the level of raffinose in food plants \cdot
                                                                                                                                  (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                        27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ۳
     sense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60
                                                           1999-593144/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                              Ē
   and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 36-38; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              572 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                0eda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       food plants
                                                                                                                                                                         98JP-0120550.
98JP-0120551.
98JP-0345590.
98JP-0351246.
                                                                                                                                                                                                                                                                      99EP-0107430
                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 210
                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mustard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.1%;
87.1%;
                                                                                                                                                                                                                                                                                                                                                                                   "encoded by ACR"
genes, useful for altering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 508; DB 20; Pred. No. 3.4e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 572;
 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
 level
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 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT 8
AAW57886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
This sequence represents the broad bean raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffino combining a D-galactosyl group through an alpha (1-6) bond with a
                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (claimed). These genes may be used to control the levels of raffinose produced in plants. Antisense genes can be used to knock out existing gene activity, and sense genes to increase the level of gene activity. The resulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, providing general health advantages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D-glucose residue in a sucrose molecule to form raffinose. cDNA (see AA220209) encoding the enzyme was isolated from mustard (Brassica juncea) leaf cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see AA220207-10) may be used to obtain other raffinose synthase genes by labeled detection or amplification
                                                                         capable of producing raffinose, used as food
beneficial effects on gastrointestinal flora
                                                                                        New nucleic acid molecule encoding plant raffinose capable of producing raffinose, used as food additi
                                                                                                                                              WPI; 1998-324670/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents mustard raffinose synthase, a protein that can bind a D-galactosyl group through an alpha(1-6) bond to the hydroxy group attached to the carbon atom at the 6-position of the
                                                                                                                                  N-PSDB; AAV40800
                                                                                                                                                                      Oeda K,
                                                                                                                                                                                                                                                                            24-JUN-1998
                                                                                                                                                                                                                                                                                                    EP849359-A2
                                                                                                                                                                                                                                                                                                                            Vicia
                                                                                                                                                                                                                                                                                                                                                      gastrointestinal flora; broad bean.
                                                                                                                                                                                                                                                                                                                                                               Raffinose synthetase;
                                                                                                                                                                                                                                                                                                                                                                                           Broad
                                                                                                                                                                                                                                                                                                                                                                                                                    23-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW57886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW57886 standard;
                                                                                                                                                                                              (SUMO)
                                                                                                                                                                                                                         18-DEC-1996;
                                                                                                                                                                                                                                                 18-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                            faba.
                                                                                                                                                                                                                                                                                                                                                                                           bean raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88;
                                                                                                                                                                                               SUMITOMO CHEM CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                    Page 26-29;
                                                                                                                                                                       Wantanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        777 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       food plants
                                                                                                                                                                                                                         96JP-0338673
                                                                                                                                                                                                                                                 97EP-0122417
                                                                                                                                                                      田
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                   44pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.7%;
87.1%;
                                                                                                                                                                                                                                                                                                                                                                                          synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55pp;
                                                                                                                                                                                                                                                                                                                                                                  metabolism modification; food
                                                    English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 506; DB Pred. No. 9.4e 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; DB 20;
. 9.4e-56;
                                                                                         finose synthetase additives with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                  additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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RESULT 9
AAY30142
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                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides in the host organism or cell is changed. Raffinose oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
                                                                                                                                         Sequence
                                                                                                                                                              The present sequence represents a raffinose synthase protein. The sequence is isolated from plant material of broad beans. The protein forms raffinose by complexing alpha(1 to 6). D-galactosyl hydroxyl group of the 6C of D-glucose residue in sucrose molecules
                                                                                                                                                                                                                          Claim 5;
                                                                                                                                                                                                                                                New raffinose synthase gene - is prepared from
                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                    WPI; 1999-511112/43.
                                                                                                                                                                                                                                                                                                                                   28-NOV-1997;
18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                             10-AUG-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                   JP11215984-A
                                                                                                                                                                                                                                                                                                                                                                                                                                           Vicia faba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY30142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY30142 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                          (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                                      12-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         589 TRDCLFEDPLHNGKTMLKIWNLNKYTGVLGLFNCQGGGWC 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      529
 589
                                              529
                      19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60
                                            TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDWDMFQSTHPCAEFHAASRAISGGPIYVSDCVGNHNFKLLKSLVLPDGSILRCQHYALP 588
           TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWC 100
TRDCLFEDPLHNGKTMLKIWNLNKYTGVLGLFNCQGGGWC
                                                                                          88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88;
                                                                                                       Similarity
                                                                                                                                                                                                                                                                        AAZ10001.
                                                                                                                                                                                                                          Page 19-21; 40pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  799 AA;
                                                                                                                                         799 AA;
                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                   97JP-0329006.
96JP-0338673.
                                                                                                                                                                                                                                                                                                                                                                      97JP-0342899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of a raffinose synthase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                      89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 broad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                799
                                                                                          Score 505; DB 20;
Pred. No. 1.3e-55;
5; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 505; DB 19;
Pred. No. 1.3e-55;
5; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                bean;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sucrose;
 628
                                                                                                                                                                                                                                                 Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 799;
                                                                                                                Length 799;
                                                                                                                                                                                                                                                 plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                           Indels
                                                                                                                                                                                                                                                 material
                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                          Gaps
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                                              588
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RESULT 10
AAB98659
ID AAB98
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AAW57887
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                                                                                                                                                                                                                                                                В
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                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a mutant protein of raffinose synthas in which at least one aromatic amino acid present at the position of about 1-7 amino acids from the N-terminus 1s deleted or replaced. The mutant protein can be used for reducing the raffinose oligosaccharide content in a plant body. The present protein from soybean, was used in the present invention.
                               Glycine max
                                                                                                                                                           AAW57887 standard;
                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel mutant protein of raffinose synthase is useful for reducing the raffinose oligosaccharide content in a plant body \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAH27438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-313373/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JUL-2000; 2000JP-0200571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP2001078783-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plant; soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soybean protein:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB98659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB98659 standard; protein; 780 AA.
         EP849359-A2
                                                     gastrointestinal flora;
                                                               Raffinose synthetase; metabolism
                                                                                      Soybean raffinose synthetase.
                                                                                                              23-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SUMO ) SUMITOMO CHEM
                                                                                                                                                                                                                                                                510
                                                                                                                                                                                                                 570 TRDCLFEDPLHDGKTMLKIWNLNKYTGVLGLFNCQGGGWC
                                                                                                                                                                                                                                        61 TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWC 100
                                                                                                                                                                                                                                                                        1 PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60
                                                                                                                                                                                                                                                               PDWDMFQSTHPCAEFHAASRAISGGPIYVSDCVGKHNFKLLKSLALPDGTILRCQHYALP 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       max.
                                                                                                                                                                                                                                                                                                                                                         780 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 18-20; 30pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99JP-0196036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ
                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                       88.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CO LTD
                                                    soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        synthase; raffinose oligosaccharide
                                                                                                                                                           781
                                                                                                                                                                                                                                                                                                                       Score 498; DB 2: Pred. No. le-54;
                                                                                                                                                           Å
                                                                                                                                                                                                                                                                                                            Mismatches
                                                                modification;
                                                                                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                  609
                                                                food additive;
                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       raffinose synthase
                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reduction;
                                                                                                                                                                                                                                                                                                           Gaps
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RESULT 12
AAY30143
     AC XXX AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
New raffinose synthase
                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the soybean raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides in the host organism or cell is changed. Raffinose oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
                                                                                                                                                                                     28-NOV-1997;
18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                           JP11215984-A
                                                                                                                                                                                                                                                                                                                                                                                                                                Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of a raffinose synthase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY30143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY30143 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
                                                                                                                                    (SUMO ) SUMITOMO CHEM
                                                                                                                                                                                                                                                                     12-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 31-34; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAV40801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0eda
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                                                                                                                                                                                                                                                                                                                       10-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SUMO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                  1999-511112/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRDCLFEDPLHDGKTMLKIWNLNKYTGVLGLFNCQGGGWC 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDWDMFQSTHPCAEFHAASRAISGGPVYVSDCVGKHNFKLLKSLALPDGTILRCQHYALP 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1998-324670/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85;
                                                         AAZ10002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMITOMO CHEM CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      781 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                     97JP-0329006.
96JP-0338673.
                                                                                                                                                                                                                                                                     97JP-0342899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plant; sucrose; raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.1%;
                                                                                                                                    CO LTD
gene
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Pred. No. 1.4e-54;
8; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   781
  is
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prepared
  from
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plant material
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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511

61

TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWC

Qy

PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP PDWDMFQSTHPCAEFHAASRAISGGPVYVSDCVGKHNFKLLKSLALPDGTILRCQHYALP

Conservative

8;

Indels

0;

Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
 Query Match
Best Local Similarity
Matches 85; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                        The present invention provides novel plant promoters which can be the production of transgenic plants which express genes with desir
                                                                                                                              with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a raffinose synthase protein. The sequence is isolated from plant material. The protein forms raffino by complexing alpha(1 to 6)- D-galactosyl hydroxyl group of the 6C of D-glucose residue in sucrose molecules.
                                          Sequence
                                                               properties
                                                                                                                                                                                                                                      30-APR-1999;
01-SEP-1999;
                                                                                                                                                                                                                                                                                                                                   Glycine
                                                                                                                                                                                                                                                                                                                                                                                                 07-MAR-2001
                                                                                                       Example 6; Page 24-27;
                                                                                                                                      New soybean plant promoters useful for generating transgenic
                                                                                                                                                             N-PSDB; AAC89523
                                                                                                                                                                                           Ishige F,
                                                                                                                                                                                                                                                                    27-APR-2000; 2000EP-0108962
                                                                                                                                                                                                                                                                                          02-NOV-2000
                                                                                                                                                                                                                                                                                                               EP1048733-A2
                                                                                                                                                                                                                                                                                                                                                        Plant promoter;
                                                                                                                                                                                                                                                                                                                                                                            Soybean raffinose synthase
                                                                                                                                                                                                                                                                                                                                                                                                                      AAB49400;
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB49400 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                 (SUMO ) SUMITOMO CHEM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60
                                                                                                                              desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDWDMFQSTHPCAEFHAASRAISGGPVYVSDCVGKHNFKLLKSLALPDGTILRCQHYALP 570
                                                                                                                                                                       2001-104537/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Page 25-27; 40pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                           Watanabe
                                           781 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          781 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                            properties
                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                      99JP-0124527.
99JP-0247211.
                                                                                                                                                                                                                                                                                                                                                      transgenic plant; desired property.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                             Ħ
           88.1%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.1%;
85.0%;
                                                                                                       36pp;
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Score 497; DB
Pred. No. 1.4e
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                        English
                                                                                                                                                                                             Χ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 497; DB 20;
Pred. No. 1.4e-54;
8; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                          ÃA
          DB 22;
                     Length 781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 781;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                           desired
                                                                                                                                        plants
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RESULT 15
AAY32073
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Best Local
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70978
                                                                                                                                                                                                                                                                                                    The present sequence is a raffinose synthase from clone sfl1.pkl25.d4 isolated from a soybean immature flower cDNA library sfl1. Raffinose synthase is involved in the biosynthesis of raffinose and higher homologues in the raffinose saccharide family from sucrose. The present sequence is useful for reducing the raffinose saccharide content of soybean seeds which improves the nutritional quality of the soy protein products derived from them.
                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids and encoded proteins involved in the biosynthesis raffinose, useful for producing soybean seeds with a reduced racontent and therefore improved nutritional quality -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycine max
         Sugarbeet raffinose synthase
                                 17-JAN-2000
                                                        AAY32073
                                                                             AAY32073 standard; Protein;
                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 47-49; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-350754/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Allen SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DUPO ) DU PONT DE NEMOURS &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200024915-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soybean; raffinose synthase; raffinose saccharide; clone sfll.pkl25.d4; nutritional; soy protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soybean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY70978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY70978 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              571
                                                                                                                                        547
                                                                                                                                                                                     487
                                                                                                                                                              61
                                                                                                                                                                                                                                             Local
                                                                                                                                                   TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR 101
                                                                                                                                                                                                PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRDCLFADPLHDGKTMLKIWNINKYTGVLGVFNCQGGGWFR 587
                                                                                                                                                                                  PDWDMFQSTHPCAAFHAASRAISGGPIYISDTVGNHNFELLKTLALPDGSILRCEHYALP 546
                                                                                                                                                                                                                                   85;
                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hitz WD;
                                                                                                                                                                                                                                                                                758 AA;
                                                                                                                                                                                                                                 Conservative
                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0105451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US24923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            synthase from clone sfll.pkl25.d4
                                                                                                                                                                                                                                           87.6%;
                                                                              783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   758
                                                                                                                                                                                                                                 9;
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Pred. No. 3.2e-54;
9; Mismatches 7;
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                                                                                                                                                                                                                                                      Length 758;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   sis of raffinose
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Search completed: March Job time: 72.439 secs

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2003, 10:03:45

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Best Local S
Matches 84
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30-APR-1998;
04-DEC-1998;
                                                                                                                                                                                  haming leaf cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see AAZ20207-10) may be used to obtain other raffinose synthase genes by labeled detection or amplification (claimed). These genes may be used to control the levels of raffinose produced in plants. Antisense genes can be used to knock out existing gene activity, and sense genes to increase the level of gene activity. The resulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, providing general health advantages.
                                                                                                                                                                                                                                                                                                     This sequence represents sugarbeet raffinose synthase, a protein that can bind a D-galactosyl group through an alpha(1-6) bond to thydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. CDNA (see AAZ20208) encoding the enzyme was isolated from sugarbeet cv.
                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                               New sense and antisense genes, useful for altering the level
                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAZ20208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-593144/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raffinose synthase; sugarbeet; transgenic plant.
                                                   570
                          61
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             TRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCR 101
TKDCLFVDPLHDGKTMLKIWNLNKYNGVLGVFNCQGGGWSR
                                                                 PDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vulgaris
                                                                                                                                                                                                                                                                                                                                                                                        25; Page 22-24;
                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  in food plants
                                                                                                                                                             783 AA;
                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oeda K;
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98JP-0345590
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                                                                                                                   84.4%;
                                                                                                                                                                                                                                                                                                                                                                                      55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "encoded by
                                                                                                                   Score 476; DB 20; Pred. No. 6.8e-52;
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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Maximum DB seq length: 2000000000
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Perfect score:
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                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237916 seqs, 58723674 residues
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDWDMFQSTHPCAAFHAASR.....LNKFTGVIGAFNCQGGGWCR 101
                                                           /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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253.439 Million cell updates/sec
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and is derived by analysis of the total score distribution. score greater Pred. No. is the number of results predicted by chance to have a ater than or equal to the score of the result being printed.

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10.5	10.5	10.5	10.6	10.7	11.0	11.2	11.2	11.2	11.2	11.2	11.3	11.4	11.4	11.9	12.1	12.2	15.1	15.1	Query Match
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US-09-934-900-6	US-09-815-837-41	US-09-815-837-17	US-10-078-770-102	US-09-960-226-4	US-09-847-172-44	US-10-054-295-55	US-10-053-758-55	US-09-438-486-55	US-09-766-253-55	US-09-843-676-55	US-10-081-281-93	US-10-047-539-2	US-09-801-368-148	US-10-043-487-266	US-09-815-242-5100	US-09-738-626-4624	US-09-847-172-23	US-09-858-580-23	ID
	•	Sequence 17, Appl	1	Sequence 4, Appli		Sequence 55, Appl	Sequence 55, Appl	Sequence 55, Appl	55,	Sequence 55, Appl	Sequence 93, Appl	Sequence 2, Appli	Sequence 148, App	Sequence 266, App	Sequence 5100, Ap	Sequence 4624, Ap	Sequence 23, Appl	Sequence 23, Appl	Description

RESULT 2 US-09-847-172-23 : Sequence 23, Application US/09847172 : Publication No. US20030007978A1

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10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.3	10.3	10.3	10.4	10.4	10.4	10.4	10.4	10.4	10.5
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US-10-097-065-157	US-09-771-161A-213	US-09-771-161A-212	US-09-977-269-11	US-09-977-261-11	US-09-977-260-11	US-09-771-161A-122	US-09-920-552-53	US-09-920-552-56	US-09-738-626-6820	US-09-815-837-46	US-09-815-837-37	US-09-815-837-22	US-09-815-837-13	US-09-809-715-4	US-09-764-869-1096	US-10-108-605-185	US-09-815-242-13951	US-09-896-301-6	US-09-977-269-12	US-09-977-261-12	US-09-977-260-12	US-10-078-770-116	US-10-078-770-108	US-09-989-919-84	US-09-934-900-12
157	Sequence 213, App	Sequence 212, App	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 122, App	Sequence 53, Appl	Sequence 56, Appl	Sequence 6820, Ap	Sequence 46, Appl	Sequence 37, Appl	Sequence 22, Appl	Sequence 13, Appl	Sequence 4, Appli	Sequence 1096, Ap	Sequence 185, App	Sequence 13951, A	Sequence 6, Appli	e 12	Sequence 12, Appl	Sequence 12, Appl	Sequence 116, App	æ	Sequence 84, Appl	•

ALIGNMENTS

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; TYPE: PRT
; ORGANISM: Mus sp.
US-09-858-580-23
                                                                                                                                                                                                                                                                                                                                                                          CURRENT EPILING DATE: US/09/858,580
CURRENT ETILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/153,586
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/064,552
PRIOR APPLICATION NUMBER: 60/064,555
PRIOR FILING DATE: 1997-09-16
PRIOR APPLICATION NUMBER: 60/064,555
PRIOR FILING DATE: 1997-10-10
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
US-09-858-580-23
US-09-858-580-23, Application US/09858580; Patent No. US20020176864A1; GENERAL INFORMATION:
; APPLICANT: BUTTOWS et al.
                                                                                                                                                     Query Match
Best Local Similarity 26.2
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver.
SEQ ID NO 23
LENGTH: 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Burrows et al.
TITLE OF INVENTION: Recombinant MHC molecules useful for manipulation of TITLE OF INVENTION: antigen-specific T-Cells ETILE REFERENCE: 48823
132 -- IWRLEEF-AKFASFEAQG 148
                                     77 LKIWNLNKFTGVIGAFNCQG 96
                                                                                73 DTVCRHNYEIFDNFLVPRRVEEHTIIQAEFYLLPDKRGEFMFDFDGDEIFHVDIEKSET- 131
                                                                                                                     31 DSVGKHNEDLLKKLVLP----DGSILRSEYYALPTR------DCLFEDPLHNGETM 76
                                                                                                                                                                                 15.1%;
26.2%;
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Pred. No. 0.02
L8; Mismatches
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0.022;
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; ORGANISM: Corynebacterium glutamicum US-09-738-626-4624
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                                                                                                                                SOFTWARE: PatentIn ver.
SEQ ID NO 4624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.1 SEQ ID NO 23
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APPLICANT: OREGON HEALTH AND SCIENCES UNIVERSITY
APPLICANT: BURROWS, GREGORY G.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4624, Application US/09738626 Publication No. US20020197605A1
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Best Local Similarity
                                                                                                                                                                                      PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: JP 99/377484 PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
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CURRENT FILING DATE: 2001-05-01
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                                                                                                                                                                        NUMBER OF SEQ ID NOS: 7059
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                                                                                                 TYPE: PRT
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                                                                                                                ENGTH: 426
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YOKOI, HARUHIKO
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26.2%; Pred. No.
 12.2%;
27.6%;
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Pred.
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 No.
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                 Length 426;
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US-10-043-487-266
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                                                                                                                 GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
APPLICANT: Pierre, LEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 5100
LENGTH: 183
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                                                                                                                                                                       Sequence 266, A Publication No.
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                                                     APPLICANT: Pierre, LEGRAIN
TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypep
TITLE OF INVENTION: mammalian polypeptides
FILE REFERENCE: B4778A
CURRENT APPLICATION NUMBER: US/10/043,487
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/261,130
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PRIOR TILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Pseudomonas aeruginosa
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Pred. No. 2;
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                                                                                                                                                                                                            Query Match
Best Local Similarity 20...
24; Conservative
Sequence 2, Application US/10047539 Patent No. US20020177547A1
                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.0
SEQ ID NO 148
LENGTH: 358
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
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SEQ ID NO 266
LENGTH: 1138
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Best Local :
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Patent No. US200
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NUMBER OF SEQ ID NOS: 561
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PRIOR FILING DATE: 2000-01-19
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CURRENT FILING DATE: 2001-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Summers, Eric TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi FILE REFERENCE: 109272.147
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                                                                                                  236 ELSETP----
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                                                                                                                                 64 CLFEDPLHNGETMLKIWNLNKFTGVIGAFNC 94
                                                                                                                                                                                               15 FHAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSI-----LRSEYYAL----PTRD 63
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Madden, Kevin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hecht, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Royer, John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 67; DB
Pred. No. 27;
                                                                                                                                                                                                                                              Score 64.5;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                               Mismatches
                                                                                                 254
                                                                                                                                                                                                                                                               DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27;
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                                                                                                                                                                                                                                                              Length 358;
                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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RESULT 8
US-10-081-281-93
; Sequence 93, Application US/10081281
; Patent No. US20020151707A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT; ORGANISM: Mus musculus US-10-047-539-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: MOLLING, I
APPLICANT: PAVLOVIC
APPLICANT: NAWRATH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS FOR TREATING OR PREVENTING FILTE OF INVENTION: CANCER FILE REPERIOR: VOS-27 CURRENT APPLICATION NUMBER: US/10/047,539 CURRENT FILING DATE: 2002-01-15 PRIOR APPLICATION NUMBER: EP 01 10 0914.9 PRIOR APPLICATION NUMBER: EP 01 10 0914.9 PRIOR FILING DATE: 2001-01-16 NUMBER: FILING DATE: 2001-01-16 NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 TIINGSQVWGGQPVYPQEPDDACVFPDGGPCPSGPKPPKRSFVYVWKTWGKYWQVLG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 PEWTEVQGSNCWRGGQVSLRVINDGPTLVGANASFSIALH-FPGSQK-VLPDGQVIWANN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity es 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PDWDMFQSTHPCAAFHAASRAISGGPIYV----SDSVGKHNFDLLKKLVLPDGSIL---- 52
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sheppard, Paul TITLE OF INVENTION: Immune Mediators and Related Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kindsvogel, Wayne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----ETMLKIWNL-NKFTGVIG
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NAWRATH, MICHAEL
                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: <Unknown>
NAME: Parent,
                                          APPLICATION NUMBER: US 60/005,964 FILING DATE: 27-0CT-1995 APPLICATION NUMBER: US 08/657,581 FILING DATE: 07-JUN-1996
                                                                                                                                   APPLICATION NUMBER: US 08/483,241 FILING DATE: 07-JUN-1995
                                                                                                                                                                             APPLICATION NUMBER: US/09/261,811A
FILING DATE: 03 Mar-1999
APPLICATION NUMBER: US 08/480,002
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/482,133
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/081,281 FILING DATE: 20-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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24.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 64.5; DE Pred. No. 26; 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42;
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TOPOLOGY: linear;

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-081-281-93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 55, Application US/09843676 Patent No. US20020164786A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 93: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 KKET----VWRLEEF-GRFASFEAQG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 DTYCRHNYGVVESFTVQRGASAGIKEEHVIIQAEFYLNPDQSGEFMFDFDGDEIFHVDMA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 NGETMLKIWNLNKFTGVIGAFNCQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 DSVGKHNFDLLKKLVLPDGS------ILRSEYYALPTR------DCLFEDPLH 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                   TELECOMMUNICATION INFORMATION
                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Andrews, William H.
TITLE OF INVENTION: No. US20020164786A1el Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 014058-005630US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                     APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997 APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997 APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/843,676 FILING DATE: 26-Apr-2001 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                       NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/854,050 FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 576-020
TELEFAX: (415) 576-0300
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend and Crew LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 42,058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cech, Thomas R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morin, Gregg B.
Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  California
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Nakamura, Toru
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Pred. No. 8.8;
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US-09-766-253-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-843-676-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 55, Application US/09766253 Publication No. US20020187471A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                        INFORMATION FOR SEQ ID NO: 55: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               499 PTQIADRIKEFKQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKDALKNENGFF 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 559 VRSQYFFNTNTGVLKLFN 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 MLKIWNLNKFTGVIGAFN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 PIYVSDSVGKHNFDLLKKL--VLPDGSIL----RSEYYALPTRDC--LFEDPL--HNGET 75
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 55:
                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Andrews, William H. TITLE OF INVENTION: No. US20020187471Alel Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide SEQ ID NO: 55:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                      NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/846,017 FILING DATE: 1997-04-25
                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 19-Jan-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acids
                                        TOPOLOGY: not relevant
                                                               STRANDEDNESS: not relevant
                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States of America
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                                                                                                     LENGTH: 884 amino acids
                                                                                                                                                                                   TELEPHONE: (415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
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                                                                                amino acid
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Harley, Calvin
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Chapman, Karen B.
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                                                                                                                                                             (415) 576-0300
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29.5%;
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                                                                                                                                                                                     576-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 884;
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Best Local Similarity
Matches 23; Conserv
                                                                                                        TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
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CLASSIFICATION: 53b
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
APPLICATION NUMBER: 18-APR-1997
776 DATE: 18-APR-1997
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STATE: Co.
COUNTRY: United
TD: 94111-3834
TD: TPADABLE F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Harley, Carring H.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US20030009019Alel Telomerase
TITLE OF SPOUENCES: 223
                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 12-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 18-APR-CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Two Embarcac
CITY: San Francisco
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   STRANDEDNESS:
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                                                                      ENGTH:
                                         amino acid
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Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
                                                                      884 amino acids
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not relevant
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; TOPOLOGY: not releval; MOLECULE TYPE: peptide US-09-438-486-55
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Best Local S
Matches 23
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                                                                                                                             INFORMATION FOR SEQ ID NO: 55: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                559 VRSQYFFNTNTGVLKLFN 576
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APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 55:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                      STRANDEDNESS: NO. US20030032075A1 Relevant
                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/854,050 FILING DATE: 09-MAY-1997 APPLICATION NUMBER: US 08/851,843 FILING DATE: 06-MAY-1997 APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997
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STATE: California
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                                                                                                                                                                        TELEFAX:
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                                                                                                    LENGTH: 884 amino acids
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Morin, Gregg B.
Harley, Calvin
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Nakamura, Toru
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29.5%;
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Pred. No.
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                                                            ; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-054-295-55
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US-10-054-295-55
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     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 55, Application US/100 Publication No. US20030044953A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                 TELEFAX: (415) 576-0 INFORMATION FOR SEQ ID NO: 55:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              559 VRSQYFFNTNTGVLKLFN 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    499 PTQIADRIKEFKQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKDALKNENGFF 558
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                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andrews, William H. TITLE OF INVENTION: No. US20030044953Alel Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                         NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                 STRANDEDNESS: No. US20030044953A1 Relevant
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/854,050 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/054,295 FILING DATE: 18-Jan-2002
                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                           LENGTH: 884 amino acids
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
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Nakamura, Toru
Chapman, Karen B.
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Harley, Calvin
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Pred. No.
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Pred.
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DB
59;
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                       9;
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                         Length 884;
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; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-172-44
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CURRENT FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: US 60/200,942
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 09/153,586
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: US 60/064,555
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: US 60/064,552
PRIOR FILING DATE: 1997-09-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-847-172-44
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                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09960226 Patent No. US20020172670A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                  SEQ ID NO 4
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                                                        CURRENT APPLICATION NUMBER: US/09/960,226
CURRENT FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/263,458
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: US 60/234,879
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                               APPLICANT: Rose, David
APPLICANT: Kuntz, Douglas
APPLICANT: Van Den Elsen, Jean
APPLICANT: Van Den Elsen, Jean
TITLE OF INVENTION: MANNOSIDASE STRUCTURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: VANDENBARK, ARTHUR A.
TITLE OF INVENTION: RECOMBINANT MHC MOLECULES USEFUL FOR MANIPULATION OF ANTIGEN-S
TITLE OF INVENTION: CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                        SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                          FILE REFERENCE: 12243.19USU1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 899-58137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: OREGON HEALTH AND SCIENCES UNIVERSITY
LENGTH: 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 T---VWRLEEF-GRFASFEAQG
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Q93XK2
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Q9SYJ4
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ALIGNMENTS

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O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-MAY-2002 (TrEMBLrel. 20, Last annotation update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)

Cucumis sativus (Cucumber).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Cucumhs.

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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF073744; AAD02832.1; -.
Glycosyltransferase; Transferase.
SEQUENCE 784 AA; 86920 MW; 3B06A491F0908933 CRC64:
121
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                                                                    PVSVGCFVGFDASEPDSRHVVSIGKLKDIRFMSIFRFKVWWTTHWVGRNGGDLESETQIV 120
ILEKSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGD
       ILEKSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGD 180
                                                                                                                   Similarity
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                                                      "Structural analysis of Arabidopsis Sequence features of the regions of physically assigned Pl clones."; DNA Res. 4:291-300(1997).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
   Southwick A., Palm C.J., Bo
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                                                                                          KKLILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPIGLVNMLNTSGAIQSVDYD
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SEQUENCE 798 AA; 88717 MW; BD3F3ED5BF8617B7 CRC64;
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                      LKFQENYKFRDYVNPKATGPRAGQKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQ 343
                                                                                     TVHPQGVIEGVRHLVDGGCPPGLVLIDDGWQSIGHDSDPITK--EGMNQTVAGEQMPCRL
                                                                                                                                       LESETQIVILEKSDS------GRPYVFLLPIVEGPFRTSIQPGD-DDFVDVCVESGSSKV 165
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VPGLPEARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGID
                                                                          KVHPEGVWEGVRRLADGGCPPGLVLIDDGWQSICHDDDDLGSGAEGMNRTSAGEQMPCRL
                                                                                                                          RGSVFRSAVYLHAGDDPFDLVKDAMRVVRAHLGTFRLMEEKTPPPIVDKFGWCTWDAFYL
                                                                                                                                                                            VENETQMMILDQSGTKSSPTGPRPYVLLLPIVEGPFRACLESGKAEDYVHMVLESGSSTV
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                       IKFQENYKFREY-----KGGMGGFVREMKAAFPTVEQVYVWHALCGYWGGLRPG
                                                                                                                                                                                                                                                                                                                                                                              AP003282; BAB64768.1; -.
NCE 816 AA; 89588 MW;
                                                                                                                                                                                                                                                                                                                                        Similarity
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59.68;
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                                                                                                                                                                                                                                                                                                                             Score 2643; DB 10;
Pred. No. 2.1e-206;
1; Mismatches 150;
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Best Local S
Matches 379
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Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 20, Last annotation update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Stachyose synthase (EC 2.4.1.67).
STS1.
Pisum sativum (Garden pea).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidaeurosids I; Fabales; Fabaceae; Papillionoideae; Vicieae; Pisum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peterbauer
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                                             VGRNGGDLESETQIVILEKSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKV 165
                                                                                              SESNAPPSLLQKVLAYSHKGGFFGFSHETPSDRLMNSIGSFNGKDFLSIFRFKTWWSTQW
                                                                                                                                                                                               MAPPLNSTTSNLIKTESIFDLSE-----RKFKVKGFPLFHDVPENV--SFRSFSSICKP
                                                                                                                                                                                                                                             {\tt MAPSFKNGGSNVVSFDGLNDMSSPFAIDGSDFTVNGHSFLSDVPENIVASPSPYTSIDK--}
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                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                         GCFVGFDASEPDSRHVVSIGKLKDIRFMSIFRFKVWWTTHW
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Q9SBZ0;
Q1SBZ0;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2000 (TrEMBLrel. 20, Last annotation update)
Q1-MAR-2002 (TrEMBLrel. 13, Last sequence (EC 2.4.1.67).
Phaseolus angularis)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidueurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae; Vigna.
                                                     SEQUENCE FROM N.A.
MEDLINE=20117502; PubMed=10652123;
MEDLINE=20117502; PubMed=10652123;
Methan J., Mayer U., Popp M., Gloessl J., Richter Peterbauer T., Mucha J., Mayer U., Popp M., Gloessl J., Richter "Stachyose synthesis in seeds of adzuki bean (Vigna angularis):
"Stachyose synthesis in seeds of adzuki bean (Vigna angularis):
"Stachyose syntha"
               molecular cloning and functional
plant J. 20:509-518(1999).
EMBL; Y19024; CAB64363.1; Glycosyltransferase; Transferase.
                                                                                                                                                                                         NCBI_TaxID=3914;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLHNGETMLKIWNLNKFTGVIGAFNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FAPIGLVNMLNTSGAIQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRACRIDGEDVGFKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QKEETSHLGKAEEYVVYLNQAEELSLMTLKSEPIQFTIQPSTFELYSFVPVTKLC-GGIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGENPISIEGVKTFALYLYQAKKL-ILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLFDHTTVLKIWNFNKYGGVIGAFNCQGAGWDPIMQKFRGFPECYKPIPGTVHVTEVEWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THPCAAFHAASRAISGGPIYVSDSVGKHNEDLLKKLVLPDGSILRSEYYALPTRDCLFED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKVGIDGVKIDVIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AESGITGVKVDVIHSLEYVCDEYGGRVDLAKVYYEGLTKSIVKNFNGNGMIASMQHCNDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGVRPETTHL-DTKIVPCKLSPGLDGTMEDLAVVEISKASLGLVHPSQANELYDSMHSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKIKKVVKEIDDLFGGEQFSSGEKSEMKSEYGLKAFTKDLRTKFKGLDDVYVWHALCGAW
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AA;
94949
MW;
 85248C4B81165679
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                                                                                                              Richter
                                                                         synthase;.";
                                                                                                                                                                                                                                Rosidae;
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RESULT 7

QBRW08

ID QBRW08

AC QBRW08;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
E Stachyose synthase (EC 2.4.1.67).
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Best Local Similarity
Matches 370; Conserv
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                                                                                                                                                                                IQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRACRIDGEDVGFKYDQDQMVVVQVPWPID
                                                                                                                                                                                                                   VYLNOAEVLHLMTPVSEPLQLTIQPSTFELYNFVPVEKLGSSNIKFAPIGLTNMFNSGGT
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                                                                                                                                                                     IQELEYIE--KDVKVKVKGGGRFLAYSTQSPKKFQLNGSDAAFQWLPDGKLTLNLAW-IE
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Pred. No. 5.8e-147;
39; Mismatches 243;
                 update)
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Best Local S
Matches 366
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stachys sieboldii.";
submitted (AUG-2001) to the EMBL/GenBank/DDBJ database
EMBL; AJ344091; CAC86963.1;
Transferase; Glycosyltransferase.
SEQUENCE 863 AA; 95227 MW; DD96FE666099DEFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stachys affinis.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Lamiaceae; Stachys.
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                                                           DSKTILKIWNENKYGGVVGAFNCQGAGWDPKEQRIKGYSECYKPLSGSVHVSDIEWDQKV
                                                                        GITGVKVDVIHTLEYVSENYGGRVELGKAYYKGLSKSLKKNFNGSGLISSMQQCNDFFLL
                                                                                                                                                                                                                 GIDGYKIDVIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFL
                                                                                                                                                                                                                                                 DEMFGGGGNDEKGSSKGCSDCSCKSQNSGMKAFTNDLRTNFKGLDDIYVWHALAGAWGGV
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                                                                                                                                                                                                                                                                                                                                                                      VNPKATGP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETQWIMLNLPEI-KSYAVVIPIVEGKERSALFPGKDGHVLISAESGSTCVKTTSFTSIAY
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              EATKMGEAEEYAVYLTESEKLLLTTPESDPIPFTLKSTTFEIFSFVPIKKLGQ-GVKFAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al Similarity
366; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.2%; Solitarity 42.3%; Politarity 42.3%; Politarity 143;
                                                                                                                                                                                                                                                                                                             ------RAGQKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGL
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Pred. No. 3e-1
.43; Mismatches
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Matches 366
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Q9SYJ4;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                             EU Arabidopsis sequencing px
Submitted (MAR-2000) to the
EMBL; AC007138; AAD22659.1;
EMBL; AL161493; CAB80690.1;
SEQUENCE 807 AA; 90122 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TIEMBLrel. 13, Created)
01-MAY-2000 (TIEMBLrel. 13, Last sequence update)
01-OCT-2000 (TIEMBLrel. 15, Last annotation update)
01-OCT-2000 (TIEMBLrel. 15, Last annotation update)
Putative raffinose synthase OR seed IMBIBITION pro
T7B11.23 OR AT4G01970
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; eudicotyledons; core
eurosids II; Brassicales; Brassicaceae; Arabidops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Huang E.N., Nascimento L., de la Bastide M., Habermann K., Preston R.R., Spiegel L.A., See L.H., Shah R., Matero A., O'Shaughnessy A., Rodriguez M., Shekher M., Swaby I., Schut Parnell L.D., Dedhia N.N., McCombie W.R.;

"Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M., Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M., Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N., Mewes H.W., Lemcke K., Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=CV. COLUMBIA;
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                                                                                                   MAPSFKNGGSNVVSFDGLNDM--SSPFAI-------DGSDFTVNGHSFLSDV
IVDKFGWCTWDAFYLTVHPQGVIEGVRHLVDGGCPPGLVLIDDGWQSIGHDSDPITKEGM
                                                                                                                                                                                  SIFRFKVWWTTHWVGRNGGDLESETQIVILE--KSDSGRPYVFLLPIVEGPFRTSIQPGD
                                                                                                                                                                 SLFRFKMWWSTAWIGKSGSDLQAETQWVMLKIPEIDS---YVAIIPTIEGAFRASLTPGE
                                                                                                                                                                                                                            PONVTFTPFSSHSISTDAPLPILLRVQANAHKGGFLGFTKESPSDRLTNSLGRFEDREFL
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                                          IVDKFGWCTWDACYLTVDPATIWTGVKEFEDGGVCPKFVIIDDGWQSINFDGDELDKDAE
                                                                                                                                                                                                                                                          PENIVASP-SPYTSIDKSPVSV------GCFVGFDASEPDSRHVVSIGKLKDIRFM
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44.5%;
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Pred. No. 4.5
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Matches 306
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Q40077;
01-NOV-1996 (TrEMBLrel. C
01-NOV-1996 (TrEMBLrel. C
01-DEC-2001 (TrEMBLrel. 1
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                                                                                                                                                                                                                                                                                                                             Spermatophyta; Magnoliophyta; Triticeae; Hordeum. NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=HIMALAYA;
                                                                                                                                                                                                                                                                                                                                                                       Hordeum vulgare (Barley).
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                          Heck G.R., Dorsett
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              135
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LPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGDDPFALVKEAMKIVR
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                                                         DIRFMSIFRFKVWWTTHWVGRNGGDLESETQIVILE-----
                                                                                                              DGSDFTVNGHSFLSDVPENIVASPSPYTSIDKSPVSVGCFVGFDASEPDSRHVVSIGKLK
                                         DCREMCLEREKLWWMTQRMGTSGRDVPLETQFILIEVPAAAGNDDGDSSDGDSEPVYLVM
                                                                                             DGR-LAVRGRTVLSGVPDNVTAAHAAGAGLVD-----GAFVGATAAEAKSHHVFTFGTLR
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yta; Liliopsida;
                                                                                                                                                 Score 1482; DI
Pred. No. 7.8e
28; Mismatches
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Last sequence up
Last annotation
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a; Poales; Poaceae; Pooidea
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Q43408;
Q43408;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last senotation update)
Putative imbibition protein.
Brassica oleracea (Cauliflower).
Brassica oleracea (Cauliflower).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid;
eurosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID-3712;
                                                                                                  STRAIN-CV. ALPHA BALOMA; TISSUE-ROOT TIPS; Fujlkura Y., Karssen C.K.; "Caullflower cDNA encoding a putative imbibition protein."; Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases. EMBL; X79330; CAA55893.1; -. SEQUENCE 765 AA; 84084 MW; 73398603048E9B58 CRC64;
                                                                                                                                                                               SEQUENCE FROM N.A.
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                       MSSPFAIDGSDFTVNGHSFLSDVPENIVASPSPYTSIDKSPVSVGCFVGFDASEPDSRHV 80
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ITSNISVQNDNLVVQGKTILTKIPDNIILTPVAGAGSDS----
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                                                              Similarity
                                                  Conservative
                                                             34.9%;
                                                           Score 1473.5;
Pred. No. 3.9
                                                   Mismatches
                                                             9e-111;
                                                                        DB 10; Length
-GAFIGATFKQSKSLHV
                                                  Indels
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O94A08:

O1-DEC-2001 (TrEMBLrel. 19, Created)

O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)

O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)

Putative imbibition protein.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Roside eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Haysshizaki Y., Ishida J., Jones Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam I
                                                                                SEQUENCE FROM N.A.
                                                                                                          NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                            VFNCQGAGWCKETKKNQIHDTSPGTLTGSIRADDADLISQVAGEDW-SGDS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                    AFNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDI------EWHSGENPISIEGVKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RVSLTRSYQQALEASIARNFTDNGCISCMCHNTDGLY-SAKQTAIVRASDDFYPRDPAS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLGRVGDDFWCTDPSGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNQPDIVMDSLAVHGLGLVNPKKVFNFYNELHSYLASCGIDGVKVDVQNIIETLGAGLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVIHLLEMLCEDYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TQVSGLKSVVDNAK-QRHNVKQVYAWHALAGYWGGVKPAASGMEHYDSALAYPVQSPGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLP--EARVIQPVLSPGLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGWQQIENKEKDENCVVRE-----GAQFATRLVGIKENAKFQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGDDPFALVKEAMKI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FPIGVLEGLRFMCCFRFKLWWMTQRMGSCGKDIPLETQFMLLESKDEVEGNGDDAPTVYT
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                         PRELIMINARY;
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Pred. No. 5.5e-110;
7; Mismatches 249; Indels
                         PRT;
                         773
                         A
                                                                                                                                                                                                                                                                       -VEIGVKGCGEMRVFASKKPRAC
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Best Local :
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ
EMBL; AL133248; CAB66109.1; -
SEQUENCE 773 AA; 85143 MW; 0852F9E67952C8E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Benes V., Rechmann S., Borkova D., Ansorge W., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
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                                              FALYLYQAKKLILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPIGLVNMLNTSG
                                                                                        VFNCQGAGWCKETKKNQIHDTSPGTLTGSIRADDADLISQVAGEDW-SGDS------
                                                                                                                                                                               DKPGNHNFDLLRKLVLPDGSVLRAKLPGRPTRDCLFADPARDGISLLKIWNMNKFTGIVG
                                                                                                                                                                                                      DSVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETMLKIWNLNKFTGVIG
                                                                                                                                                                                                                                                                                                                                                         RVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLGRVGDDFWCTDPSGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FPIGVLEGLRFMCCFRFKLWWMTQRMGSCGKDIPLETQFMLLESKDEVEGNGDDAPTVYT
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    -IVYAYRSGEVVRLPKGASIPLTLKVLEYELFHISPL-KEITENISFAPIGLVDMFNSSG
                                                                                                                                                                                                                                                                                                                    PNGTFWLQGCHMVHCAN---DSLWMGNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVS
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85143 MW; 0852F9E67952C8D3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 6.6e-110;
7; Mismatches 249; Indels
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RESULT
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Best Local S
Matches 305
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JU
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Q8RX87;
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AY090237; AAL90901.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J., Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Sat Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                        KATGPRAGQKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLPEARVIQ-PVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DMTIKPAVRISDGNLIIKNRTILTGVPDNVITT----SASEAGPVE-GVFVGAVFNKEES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DMSSPFAIDGSD--FTVNGHSFLSDVPENIVASPSPYTSIDKSPVSVGCFVGFDASEPDS
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  GGLGGRVELTRQFHQALDSSVAKNFPDNGCIACMSHNTDALYCSKQAAVI-RASDDFYPR
                                                 EDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLGRVGDDFWCT
                                                                                                    SKGVVENDPTWKTDVMTLQGLGLVSPKKVYKFYNELHSYLADAGVDGVKVDVQCVLETLG
                                                                                                                                                        SPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVIHLLEMLC
                                                                                                                                                                                                            KKDDPNVGIKNIVKIAKEKHG----LKYVYVWHAITGYWGGVR---PGEEYGSVMKYPNM
                                                                                                                                                                                                                                                                                                                    TPPKFVIIDDGWQSVERDA-----TVEAGDEKKESPIFRLTGIKENEKFK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1446.5; DB 10; Length Pred. No. 7.2e-109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2AC8AB0EA43F8056 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Q9M4M7;
01-OCT-2000
01-OCT-2000
01-DEC-2001
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"Isolation and characterization of cDNAs for mRNAs regulated cold storage of avocado (Persea americana Mill.) fruit."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AJ133148; CAB77245.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-CV. HASS; TISSUE-MESOCARP;
Zamorano J.P. Evans A.D., Dopico B., Lowe A.L.,
Merodio C., Grierson D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Persea americana (Avocado),
Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Laurales;
NCBI_TaxID=3435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIDGSDFTVNGHSFLSDVPENIVASPSPYTSIDKSPVSVGCFVGFDASEPDSRHVVSIGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGVIGAFNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWHS----GENPISIEGVKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETMLKIWNLNKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPSGDPNGTFWLQGCHMVHCAN---DSLWMGNFIHPDWDMFQSTHPCAAFHAASRAISGG
                                                                                                               WQSIGHDSDPITKEGMNQTVA-GEQMPCRLLKFQENYKFRDYVNPKATGPRAGQKGMKAF
                                                                                                                                                                             KHLYSFQHLEKKKIPSFLDWFGWCTWDAFFTDVTDEGVEEGLKSLSGGGTPPRFLIIDDG
                                                                                                                                                                                                    THLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVHPQGVIEGVRHLVDGGCPPGLVLIDDG
                                                                                                                                                                                                                                                                                          LPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGDDPFALVKEAMKIVR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                              AIEGLRYEAEKMKVVMEVKGCGKFGSYSSVKPKRCVVESNEIAFEYDSSSGLV
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                                         IDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLP--EARVIQPVLSPGLQMTMEDLAVD
                                                                                     WQQIGSEE----TKDDSNCVVXEGAQFASRLTGIKENDKF-----QKNGKSEHVPGLKLV
                                                                                                                                                                                                                                                                   LPLLEGQFRAVLQGNESNQIEICLESGDCAVRTNQGMYLVYMHAGTNPFQVINQAVKAVE 182
                                                                                                                                                                                                                                                                                                                                                         LEGLRETCCFRFKLWWMTQRMGMCGKDVPLETQFMLIESKDGAAAIDDDEEEAPTIYTVF
                                                                                                                                                                                                                                                                                                                                                                                    TGVLGVYNCQGAAWSSTERKNIFHQTKTDSLTGSIRGRDV--HSISEASTDPTTWNG--D
VDDAK-QHHNVKFVYVWHALAGYWGGVKPPAAGMEHYDTALAYPVQSPGVMGNQPDIVMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1413.5; DB 10; Length Pred. No. 3.1e-106;
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es 268;
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RESULT
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 SEQUENCE FROM N.A.
Shinn P.P., Buehler E.E., Di
Walker M.M., Altafi H.H., A:
Gonzalez A.A., Hansen N.N.F
Lenz C.C., Li J.J., Liu S.S
                                                                                                                                                                                                                                                                                                                                                                                                  Q9LFZ7;
Q9LFZ7;
01-OCT-2000
01-OCT-2000
01-JUN-2002
F20N2.14.
                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J. Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID-3702;
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Dunn P.P., Feng J.J., Kim C.C., Li Y.Y
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F., Huizar L.L., Kremenetskaia I.I.,
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Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopso Cheuk R., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Com L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., La Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A. Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel Theologis A., Ecker J., Vaysberg M., Yu G., Davis R., Federspiel Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AC002328: AAR79504 1; -.

InterPro: IPR004798; Cax.

TIGRFAMs; TIGR00378: Cax.
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     NPISIEGVKTFALYLYQAKKLILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPI
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ALIGNMENTS

RESULT C85025

Š 멍 δ. 밁 Ş B δÃ DЪ QΥ Дb γQ ДЬ Qy В δÃ A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Recession: C85025
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-807 <570> R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Nature 402, 769-777, 1999hypothetical protein AT4g01970 [imported] - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 C;Accession: C85025 A; Map position: A; Gene: AT4g01970 A; Cross-references: Best Loc Matches Genetics: Query Match 391 351 171 151 114 SLFRFKMWWSTAWIGKSGSDLQAETQWVMLKIPEIDS---YVAIIPTIEGAFRASLTPGE 170 93 54 44 Match 43.9%; So Local Similarity 44.5%; Poses 366; Conservative 146; μ 1 MAPSFKNGGSNVVSFDGLNDM--SSPFAI-------DGSDFTVNGHSFLSDV 43 HALCGYWGGLRPQVPGLPEARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMY KGNVLICAESGSTKVKESSFKSIAYIHICDNPYNLMKEAFSALRVHMNTFKLLEEKKLPK DDFVDVCVESGSSKVVDASFRSMLYLHAGDDPFALVKEAMKIVRTHLGTFRLLEEKTPPG
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RESULT 2
$27762
$1pl protein - barley
C;Species: Hordeum vulgare (barley)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Sep-1997
C;Accession: $27762
R;Heck, G.R.; Dorsett, C.; Ho, T.H.
submitted to the EMBL Data Library, February 1992
A;Description: Cloning and characterization of a gene, Sipl, associated with A;Reference number: $27762
A;Molecule type: DNA
A;Residues: 1-757 <HECk, A;Residues: 1-7
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LVDETKKE-HGVKSVYVWHAMAGYWGGVKPSAAGMEHYEPALAYPVQSPGVTGNQPDIVM
                                                     FIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLP--EARVIQPVLSPGLQMTMEDLAV
                                                                                                                                                                 WQSIGHDS--DPITKEGMNQTVAGEQMPCRLLKFQENYKFRDYVNPKATGPRAGQKGMKA 312
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238 312 286

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probable imbibition protein - wild cabbage C;Species: Brassica oleracea (wild cabbage) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 C;Accession: S45033 R;Fujikura, Y; Karssen, C.K. submitted to the EMBL Data Library, May 1994 A;Description: Cauliflower cDNA encoding a putative A;Reference number: S45033 A;Accession: S45033
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 WQSIGH----DSDPITKEGMNQTVAGEQMPCRLLKFQENYKFRDYVNPKATGPRAGQKGMK 311
                                      ROMOTFHHREKKKLPSFVDWFGWCTWDAFYTDVTAEGVDEGLRSLSEGGTPPRFLIIDDG
                                                                     \tt THLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVHPQGVIEGVRHLVDGGCPPGLVLIDDG
                                                                                                            LPLLEGQFRAVLQGNEKNEIEICLESGDKAVGTSQGTHLVYVHAGTNPFEVITQSVKAAE
                                                                                                                                LPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGDDPFALVKEAMKIVR
                                                                                                                                                                              FPIGVLEGLRFMCCFRFKLWWMTQRMGASGKDIPLETQFMLLESKDEVNGDDAPTVYTVF
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                                                                                                                                                                                                                                                    ITSNISVQNDNLVVQGKTILTKIPDNIILTPVAGAGSDS-----GAFIGATFKQSKSLHV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVIHLLEMLCEDYGGRVDLAKAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGELVRLPRGATLPVTLKRLEYELFHVCPV-RAVAPGVSFAPIGLLHMFNAGGAVEECTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKKLILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPIGLVNMLNTSGAIQSVDY
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                                                                                                                                                                                                                                                                                                                         297;
                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                         Conservative 155;
                                                                                                                                                                                                                                                                                                                                          34.9%;
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. Library, May 1994
r cDNA encoding a putative
                                                                                                                                                                                                                                                                                                                                          Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       imbibition protein homolog - Arabidopsis thaliana
N;Alternate names: protein T8H10.120
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
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A; Residues: 1-773 <BEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A; Accession: T46188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: T46188
R; Benes, V.; Rechman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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A; Introns: 64/2: 146/1; 176/2; 192/3; 223/2: 259/2; 300/2; 484/3; 507/2;
                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL: AL133248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 36.6
Conservative
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   178
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                                 VRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVHPQGVIEGVRHLVDGGCPPGLVLID 252
                                                                                        FLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHAGDDPFALVKEAMKI 192
                                                                                                                                                                 VSIGKLKDIRFMSIFRFKVWWTTHWVGRNGGDLESETQIVILEK------SDSGRPYV 13:
                                                                                                                                                                                                                                                  MSSPFAIDGSDFTVNGHSFLSDVPENIVASPSPYTSIDKSPVSVGCFVGFDASEPDSRHV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D-QMVVVQVP 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---HTIHIASVAYNTLFLGEFMQPDWDMFHSLHPTAEYHAAARAVGGCAIYVSDKPGNHN
                                                                      VFLPLLEGQFRAVLQGNEKNEIEICFESGDKAVETSQGTHLVYVHAGTNPFEVIRQSVKA 177
                                                                                                                                          FPIGVLEGLRFMCCFRFKLWWMTQRMGSCGKDIPLETQFMLLESKDEVEGNGDDAPTVYT 117
                                                                                                                                                                                                             ITSNISVQNDNLVVQGKTILTKIPDNIILTP-----VTGNGFVSGSFIGATFEQSKSLHV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTVTDEKPELSSSSVVSENRSPTALISLGVRGCGRFGAYSSQRPLRCAVDGTETEFNYDA 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKKLILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPIGLVNMLNTSGAIQSV---; :| :| |:|| :|| |:|| |:|| |:||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GWCKDTKKNRIHDTSPGTLTGLVRAEDADLISEVAGQDW-GGDS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QGCHMVHCAN---DSLWMGNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVIHLLEMLCEDYGGRVDLAKA 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVGLVTLNLP 750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GWCRETRRNQCFSQYSKRVTSKTNPKDI-----EWHSGENPISIEGVKTFALYLYQ 657
VERHMOTFHHREKKKLPSFLDWFGWCTWDAFYTDVTAEGVDEGLKSLSEGGTPPKFLIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----DYDDDLSS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YHQALEASIARNFKDNGCISCMCHNTDGLY-SAKQTAIVRASDDYYPRDPAS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MDSLAVHGLGLVNPKKVFNFYNELHSYLASCGIDGVKVDVQNIIETLGAGLGGRVSLTRS
                                                                                                                                                                                                                                                                                                                                                                                                                                cultivar Columbia; BAC clone T8H10
                                                                                                                                                                                                                                                                                                      34.5%;
                                                                                                                                                                                                                                                                                    %; Score 1458.5;
%; Pred. No. 3.1e-
157; Mismatches
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                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                     249;
                                                                                                                                                                                                                                                                                     Indels 103;
                                                                                                                                                                                                                                                                                                                     Length 773;
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                                                                                                                                                                                                                                                                                                                                                                                                           FALYLYQAKKLILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPIGLVNMLNTSG
                                                                                                                                                                                               AVESTETDFTYDAEVGLVTLNLP
                                                                                                                                                                                                                                         RIDGEDVGFKYDQD-QMVVVQVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETMLKIWNLNKFTGVIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PNGTFWLQGCHMVHCAN---DSLWMGNEIHPDWDMFQSTHPCAAFHAASRAISGGPIYVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLGRVGDDFWCTDPSGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVIHLLEMLCEDYGG
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|||| | : | : : | | | | | | : : | | | : : | |
                                                                                                                                                                                                                                                                            AIESIDINHVTDKNPEFFDGEISSASPALSDNRSPTALVSVSVRGCGRFGAYSSQRPLKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDI-----EWHSGENPISIEGVKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNQPDIVMDSLAVHGLGLVNPKKVFNFYNELHSYLASCGIDGVKVDVQNIIETLGAGLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TQVSGLKSVVDNAK-QRHNVKQVYAWHALAGYWGGVKPAASGMEHYDSALAYPVQSPGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGWQQIENKEKDENCVVQE-----GAQFATRLVGIKENAKFQ-----KSDQKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----GMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLP--EARVIQPVLSPGLQ 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----HTTHTASVAYNSLFLGEFMQPDWDMFHSLHPTAEYHAAARAVGGCATYVS
                                                                                                                                                                                                                                                                                                                           -YDDDLSS-----
                                                                                                                                                                                                 758
                                                                                                                                                                                                                                                                                                                           ----VEIGVKGCGEMRVFASKKPRAC
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O.; Alon
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protein F20N2.14 [imported] - Arabidopsis thaliana
C;Specles: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: C96599
C;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; A
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewa
ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; K
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Mar
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, S.X.; Luros, J.S.; Maiti, R.; Mar
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Ta
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: C96599
A;Status nrediminary
                                                                                                                      A; Map position:
                                                                                                                                                            A; Gene: F20N2.14
                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                 A;Cross-references: GB:AE005173; NID:g8778496; PIDN:AAF79504.1; GSPDB:GN00141
                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-1170 <STO>
                                                                                                                                                                                                                                                                                                           A; Status: preliminary
         Matches
                                                           Query Match
   Local Similarity
mes 259; Conserv
      Conservative 135;
                                  27.0%;
Score 1140; DB 2;
Pred. No. 1.1e-81;
35; Mismatches 208
      208;
                                                           Length 1170;
      Indels 176;
   Gaps
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   20;
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26 AIDGSDFTVNGHSFLSDVPENIVASP-SPYTSIDKSPVSVGCFVGFDASEPDSRHVVSIG 84

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A;Cross-references: EMBL:X95875; NID:g1212811
A;Experimental source: germinating seed
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
T09530

C; Species: Cicer arietinum (chickpea, garbanzo)
C; Species: Cicer arietinum (chickpea, garbanzo)
C; Date: 16-U1-1999 #sequence_revision 16-U1-1999 #text_change 20-Jun-2000
C; Accession: T09530
C; Accession: T09530
R; Cervantes, E.
                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-357 <CER>
                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, February 1996 A; Reference number: Z16718 A; Accession: T09530
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Best Local Similarity
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       Conservative
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11.6%; Score 490.5; DB 2; 32.5%; Pred. No. 6.2e-31; tive 55; Mismatches 154;
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                                                                    Length 357;
       Indels
       55;
   Gaps
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322 KT	168 NA	271 NQ	218 CT 114 CT	158 VE : 87 LE	106 VG : 27 MG	Query Matc Best Local Matches 1	ap positi ntrons: 5 ote: A_IG	esidues: ross-refe xperiment	tatus: tr olecule t	cheet, P. mitted to escriptic eference ccession:	othetical pecies: A ate: 19-F ccession:	ULT 7	326 RA	529 RA	277 DE	472 DE		2	352 VI	02	300 AT	63 RF	247 GI	3 QC ::	187 KE
KTVEHVYVWHALCGYWGGLRPQVPGLPEARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLV 381	NADSAA-NFANRLTHIKEKHKFQKDGKEGHRVDDPALSLGHVITDIKSN- 215	ENYKFRDYVNPKATGPRAGQ	CTWDAFYLTVHPQGVIEGVRHLVDGGCPPGLVLIDDGWQSIGHDSDPITKEGM 270	VESGSSKVVDASFRSMLYLHAGDDFFALVKEAMKIVRTHLGTFRLLEEKTPDGIVDKFGW 217 	VGRNGGDLESETQIVILEKSDSGRPVVFLLPIVEGPFRTSIQPGDDDFVDVC 15	Match 11.2%; Score 471.5; DB 2; Length 371; Local Similarity 26.9%; Pred. No. 2.1e-29; Local Similarity 71; Mismatches 112; Indels 173; Gaps	A;Map position: 4 A;Map position: 5/2; 25/3; 103/3; 126/1; 174/2; 240/1; 284/1; 295/1; 333/2; 34 A;Note: A_IG002N01.5	1-371 <sch> erences: EMBL:AF007269; NID:g2191126; PID:g2191156 tal source: cultivar Columbia</sch>	ranslated from GB/EMBL/DDBJ type: DNA	R;Scheet, P.; Maggi, L. submitted to the EMBL Data Library, June 1997 submitted to the EMBL Data Library, June 1997 A;Description: The sequence of A. thallana IG002N01. A;Reference number: Z14407 A;Accession: T01717	l protein A_IG002N01.5 - Arabidopsis thaliana Arabidopsis thaliana (mouse-ear cress) Feb-1999 #sequence_revision 19-Feb-1999 #text_change 24-Mar-19 : T01717		RAIGGCOFMSVISOATTILIFLRSLVLADGS 356	AISGGPIYVSDSVGKHNFDLLKKLVLPDGS 559	DDFYPHDPASHTIHISSVAYNSLFLGEFMQPDWDMFHSLHPAAEYHAAA 32	رب ر			VIQEVISEGLQMIMBULAVURIVLIHRVGLVEPEKABERMYEGLHAHERKVGLUGVKLUVIH 411 VIQEVISEGLQMIMBULAVURIVLIH VILH 411 ATSAVTRSTWNOPDIVKDSLAVEGLRIVHPRGETSTNE-THAKLASCGVDGVKVDVOT 217		ATGPRAGQKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLPEAR 351	RFLIMTMVGNRLKVKQSKGSGCVVQEGAQLLLGDWIRDA 101	DDGWQSIGHDSDPITKEGMNQTVAGEQMPCRLLKFQENVKFRDYVNPK 2	QQAVKAVEKHMQTFHHREKKRVPSFLDWFGWCTWDAFYTDVTAEGVEEGLKSLSEGGTPP 62	EAMKIVRTHLGTERLLEEKTPPGIVDKFGWCTWDAFYLTVHPQGVIEGVRHLVDGGCPP 246
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Oy 235 GVRHLVDGGCPPGLVLIDDGWOSIGHDSDPTTKEGMNQTVAGEQMPCRLLKFQENYKF 292 : ::	Best Local Similarity 24.0%; Pred. No. 1.4e-20; Matches 156; Conservative 101; Mismatches 218; Indels 174; Gaps 32; Qy 28 DGSDFTVNGHSFLSDVPENIVASPSPYTSIDKSP 61 :::	GSIL 561	Db 216 NSLKYVYWHAITGYWGGVKPSVSGI
·	· · · · · · · · · · · · · · · · · · ·	J.; Chan - Redder, F	
Qy 294 D-YVNPKATGPRAGQKGMKAFIDEL		RESULT 9 \$76481 hypothetical protein - Synechocystis sp. (strain PCC 6803) C; Species: Synechocystis sp. A; Variety: PCC 6803 C; Species: Synechocystis sp. A; Variety: PCC 6803 C; Species: Synechocystis sp. A; Variety: PCC 6803 C; Species: Synechocystis sp. A; Variety: Poc 6803 C; Species: Synechocystis sp. A; Variety: Paper 1997 #text_change 08-Oct-1999 C; Accession: S76481 R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasana, C.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasana, C.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasana, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasana, Y.; Miyajima, O., K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasanaha, Y.; Yasa	Db 369 NOWVIHAIYDSFPIGLASRNIQIALQYSVGKDVINCMSNNPENYCN-YF 416 Qy 459 FLGTEAISLGRYGDDFWCTDPSGDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQ 516 1 1

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A;Cross-references: EMBL:AL031324; PIDN:CAA20445.1;
A;Experimental source: strain 972h-; cosmid c1672
C;Genetics:
C;Genet SpdB:SpcC1672.07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision
C;Accession: T41051
R;Hilbert, H.; Duesterhoeft, A.; Wood,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: Z21967
A; Accession: T41051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              beta transducin - fission yeast (Schizosaccharomyces pombe)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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       746
                                        610
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     RIDGEDVGFKYDQDQMVVVQVPWPIDSSSGGISVIE
                                                                                                       DDFGIRIVDVQTRKIVRELWGHSNRLTSFDFSDTGRWLVTASLDGTIRTWDLPTGHLIDS
                                                                                                                                                                         KPVTAVMLDNVNRILVTASLDGILKFWDFNKGNLIDSLDVGSSITHAIYQHSSDLVAVAC
                                                                                                                                                                                                                                             QHVLPTSDGTSVRSVCVSCCGNFGLIGSSKGVVDVYNMQSG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D-DFWCTDPSGDPNGTF---
                                        ISTPSVCTSLTFAPTG
                                                                                                                                                                                                             KRVTS - - - KTNP - - -
                                                                                                                                                                                                                                                                                                             QGSVISKAKKLNVRPEELKLPEITALSSSNTREKYWDNVLTAHKNDSSARTWNWKSKTLG
                                                                                                                                                                                                                                                                                                                                                DGSIL-----RSEYYALP-
                                                                                                                                                                                                                                                                                                                                                                                 RSRNGHYEPPSFVKFYGKSVHFLISAATDRSLRAVS---LY-QDS---
                                                                                                                                                                                                                                                                                                                                                                                                               ----GNFIHPDWDMF--QSTH--PCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLP 556
                                                                                                                                                                                                                                                                                                                                                                                                                                               DLSFWDLSKRRIQNVTYNAHFGSLPKIQFLNGQPILVTAGPDNSLKEWIFDSMDGAPRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DVLAVGTISGRI----VIFNLKNGSILMEFKQDGQVLSCSFRTD----GTPILASSNPIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMLC-EDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAI-SLGRVG 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NTNADITSLLHPSTYLNKILLGFSDGALQIWNLRVSKRVHEFQEFFG-DGITSLTQAPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLQMTMEDLAVDKIVLHKVGLVPPEKAEEMY - - - - - EGLHAHLEKVGIDGV - KIDVIHLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVEQEHGTVTHLDAFGEWIIACTSSRHVYVWKHASKY--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGHDSDPITKEGMNQTVAGEQMPCRLLKFQENYKFRDYVNPKATGPRAGQKGMKAFID- 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SFLEDTDNLPEKIVGPGQDLAYTYMKSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                      -TSLHFAPIGLVNMLNTSGAIQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85; Mismatches
                                                                                                                                                                                                                                                                                                                                              -----TRDCLFEDPL--HNGETMLKIWNLNKFT--
                                                                                                                                                                                                          KDIEWHSGENPISIEGVKTFALYLYQAKKLILSKPS
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                                                                                                                                           ALDPFEFE----
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August 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -WLQGCHMVHCA--NDSL--WM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-Dec-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.
                                    DYLATTHVDQVGISLWTNLSMFKHVSTKAL
                                                                                                                                                                                                                                                                           GVIGAFNCQGGGWCRETRRNQCFSQYS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.
                                                                                                                                         -LITVS--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        902;
                                                                                                                                       -PVTKLIQ-
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C;Genetics:
A;Gene: SGD
                                                                                                  submitted to the EMBL Data Library, A;Description: The sequence of S. co A;Reference number: S69555
                                                   A; Molecule type: DNA
A; Residues: 1-632 < DIE>
                                                                                    A; Reference number: A; Accession: S69702
                                                                                                                                                                     hypothetical protein YDR419w - yeast (Saccharomyces cerevisiae) c;Species: Saccharomyces cerevisiae C;Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change C;Accession: S69702
                                                                                                                                                                                                                                          RESULT
S69702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 273, 8205-02,,, 251-18. A:Title: cDNA cloning and expression of a : A-Peference number: Z22126; MUID:98192620;
                                    A; Cross-references:
                                                                                                                                                         R; Dietrich, F.S.
                                                                                                                                                                                                                                                                                                                                                                              Вb
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C;Superfamily: polypeptide N-acetylgalactosaminyltransferase
C;Keywords: glycosyltransferase; hexosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-623 < HAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Hagen, F.K.; Nehrke, K.
J. Biol. Chem. 273, 8268-8277, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable polypeptide N-acetylgalactosaminyltransferase (EC C;Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: T42245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: T42245
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       SGD: RAD30
                                                                                                                                                                                                                                                                                                             NQGGNQYWM
                                                                                                                                                                                                                                                                                                                                              HCANDSLWM
                                                                                                                                                                                                                                                                                                                                                                                                             --CNDF-----MFLGTEAISLGRV----GDDFWCTD--PSGDPNGTFWLQGCHMV
                                                                                                                                                                                                                                                                                                                                                                                                                                               WRTGVNVLKRNSIRLAEVWLDDY-----KTYY---YERINNQLGDFGDISSRKKLRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLFSIDKEYFEKLGTYDPGFDIWGGENLELSFKIWMCGGTLEIVPCSHVGHVFRKRSPYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVIDDNTFEYHHSKAYFTSVGGFDWGLQFNWHSIPERDRKNRTRPIDPVRSP----TMAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KILRMEKREGLIRARLRGAAVATGEVLTYLDSHCECMEGWMEPLLDRIKRDPTTVVCPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MPCRLLKFQENYKFRDYVNPKATGP-----RAGQKGMKAFIDELKGEFKTV-----
                                                                                                                                                                                                                                                                                                                                                                              LGCKSFKWYLDNIYPELFVPGESVAKGEMRNAGGKNRQCIDYKPSG--GKTVGMYQCH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKYGIDGYKIDYIHLLEMLCEDYGGRYDLAKAYYKAMTKSINKHFKGNGVIASMEH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --LAVDKIVLHKVG-
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                                    EMBL: U33007; NID: g927685; PIDN: AAB64856.1; PID: g927690; MIPS: YDR4
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                                                                                                                     // August 1995
cerevisiae la
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and

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A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae R A;Reference number: A64000; MUID:95350630; PMID:7542800 A;Accession: I64118
A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-730 <TIGR>
A;Residues: 1-730 <TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
164118
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                                                                                                                                                                                                                                                                                                                                                                                    R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Science 269, 496-512, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: 164118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1,4\text{-alpha-glucan} branching enzyme (EC 2.4.1.18) - Haemophilus influenzae (strain C:Species: Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EHVYVWHALCGYWGGLRPQVPGLPEARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVP-- 382
  VNFRLWAPNARRVSIVGDF---
                                        VGFDASEPDSRHVVSIGKLKDIRFMSIFRFKVWWTTHWVGRNGG---DLESETQIVILEK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----WCRE-TRRNQCFSQ-YSKRVTSKT----NPKDIEWHSGENPISIEGVKT 650
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                                                                                  Similarity 17.1
17; Conservative
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                                                                              2.5%; Score 105; DB 1; 17.5%; Pred. No. 7.3; ative 75; Mismatches 203
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Pred. No. 1.2;
--NYWDGRRHPMRFHSKSGVWELFLPK 181
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                                                                                203;
                                                                                                                         Length 730;
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A; Introns: 46/3; 308/3;
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A;Residues: 1-3944 <WIL>
A;Cross-references: EMBL:Z69902; PIDN:CAA93765.1; GSPDB:GN00020; CESP:C47D12.1
                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, March 1996
A;Reference number: Z19209
A;Accession: T19997
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                      A; Experimental source: clone C47D12
                                                                                Best Loc
Matches
                                                                                                                                                                                                                                    Genetics:
                                                                                                                           Query Match
2931 VVSYGHVKILQAMNLVR----
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                                        80
                                                                                Local Similarity 18.
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                                      VVSIGKLKDIRFMSIFRFKVWWTTHWVGRNGGDLESETQIVILEKSDSGRPYVFLLPIVE 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NPKDIEW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTKSINKHEKGNGVIASMEHCNDFMELGTEAISLGRVGDDFWCTDPSGDPNGTFWLQGCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARVIOPVLSPGLOMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAH-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HL-----VDGGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQMPCRLLKFQE 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLLFMGNEFAQGREWNYEESLDWFLLDENIGGGWHKGVLKLVKDLNQIYQKNRPLFELDN
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                                                                                                                                                                   408/2; 449/3; 820/3; 946/3; 1069/1; 1634/3;
                                                                                2.4%; Score 103; DB 2;
18.5%; Pred. No. 1.4e+02;
tive 90; Mismatches 230;
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-----EIEESTDIRI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                      Length 3944;
                                                                                                                                                                   1737/2; 2009/2;
                                                                                Gaps
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Search completed: April 4,
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                                                              661 LILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLH 696
                                                                                                               610 -RETRRNQCFSQYSKRVTSKTNPK------DIEWHSGENPISIEGVKTFALYLYQAKK 660
                                                                                                                                               389 QKIMTHNDFMKLSSIFSRDNARTPIP-WNSK-----GGFNDSGKSWLPYNKSFKTINVE
                                                                                                                                                                                                                513 DMFQSTHPCAAFHAASRAISGGP-IYVSDSVGKHNFDLLKKL-VLPDGSILRS-EYYALP 569
                                                                                                                                                                                                                                                                                                   227
                                                                                                                                                                                                                                                    287 GFDFIKFKKIIAQWQKDVS---NG--W-----NSLYFNNHDQPRAISRFLHDQV 330
                                                                                                                                                                  LROKTWKDDNEIMSVSESWAMNSKDVNENTNLENKAYSLTFNFDHMISEFEYVDGKKTWK 286
                                                                                                                                                                                                                                                                                                                        ------GNGVIASME------HCNDFMFLGTEAISL------GR---V 470
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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length: 2000000000
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AAW57887
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                                                                                                                                                                                                                                                             Description
                                                                                                                  Mustard raffinose
Herbicidally activ
Sugarbeet raffinos
                      Soybean raffinose
Soybean raffinose
                                                                     Soybean raffinose
Amino acid sequenc
                                                                                                                                                                                          Cucumber raffinose
Cucumber raffinose
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106	106	106.5	107	107	107	107	107	107	107	107.5	109	111	153	177.5	181	181	263.5	389.5	788	788	873	940	1384	1394	1398.5	1432.5	1470	1490	1853.5	2364	t n	2529	J	76
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22	22	22	18	17	11	23	19	23	19	20	18	13	23	21	20	19	21	21	20	19	20	21	21	20	21	21	21	21	23	20	20	19	20	19
ABG14554	AAM00803	AAB20088	AAW09043	AAR89494	AAR08257	AAU95482	AAW64169	AAU95497	AAW64182	AAY33727	AAW21636	AAR25825	ABP35067	AAG28630	AAY17422	AAW53567	AAG28629	AAG28628	AAY30145	AAW57889	AAY32072	AAY70974	AAY70976	AAY17418	AAY70981	AAY70975	AAY70977	AAY70980	ABB92806	AAY32075	AAY30144	788	2	AAW57886
Novel human diagno	Human bone marrow	Rat CARD-6 protein	Bacillus thuringle	B.t. toxin 81A2.	w	Lettuce pest resis	Lettuce resistance	Lettuce pest resis	Lettuce resistance	Photorhabdus lumin	Grapevine leafroll	Novel toxin expres		Arabidopsis thalia	Cucumber raffinose	Cucumber raffinose	Arabidopsis thalia	Arabidopsis thalla	Amino acid sequenc	Corn raffinose syn	ean raffin	raffinose	Rice raffinose syn	n raffino:		raffinose	affinose sy	Wheat raffinose sy	œ	Rapeseed raffinose	Amino acid sequenc	ese ar	acid	Broad bean raffino

ALIGNMENTS

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RESULT 1
AAW53570
Claim 3; Pages 17-20; 26pp; Japanese
                        Raffinose synthase gene - useful for preparation of raffinose in transformed plant
                                                   WPI; 1998-264858/24.
N-PSDB; AAV22250.
                                                                                                                                                              JP10084973-A.
                                                                                                                                                                                Cucumis sativus
                                                                                                                                                                                                  Cucumber; raffinose synthase; sucrose; galactinol.
                                                                                                                                                                                                                    Cucumber raffinose synthase
                                                                                                                                                                                                                                      06-JUL-1998 (first entry)
                                                                                                                                                                                                                                                         AAW53570;
                                                                                                                                                                                                                                                                          AAW53570 standard; Protein; 784 AA
                                                                                               26-JUL-1996;
26-APR-1996;
                                                                                                                           28-APR-1997;
                                                                                                                                             07-APR-1998
                                                                             (AJIN ) AJINOMOTO KK
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96JP-0107682
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RESULT 2
AAY17417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is cucumber raffinose synthase, which forms raffinose from sucrose and galactinol, has an optimum pH of 6 to 8 and working temperature of 35 to 40 degrees C, has a molecular weight of 75 to 95 kDa by gel filtration or 90 to 100 kDa by PAGE and SDS-PAGE under reductive conditions and is inhibited by
                                                                                                                                                             661
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                                                            EYLF
                                                                                                         GGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLGRVGDDFWCTDPS
                                                                                                                                                                       LILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPIGLVNMLNTSGAIQSVDYDDD
                                                                                                                                                                                                                       FNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWHSGENPISIEGVKTFALYLYQAKK
                                                                                                                                                                                                                                                                      SVGKHNFDLLKKLVLPDGSSILRSEYYALPTRDCLFEDPLHNGETMLKIWNLNKFTGVIGA
                                                                                                                                                                                                                                                                                                                     GDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVSD
                                                                                                                                                                                                                                                                                                                                                                                                    LOMIMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVIHLLEMLCEDY
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                                                                                    EYLF
                                                                                                                                                                                                                                                         SVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETMLKIWNLNKFTGVIGA
                                                                                                                                                                                                                                                                                                        GDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVSD
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                                                                                                                                                          LILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPIGLVNMLNTSGAIQSVDYDDD
                                                                                                                                                                                                          FNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWHSGENPISIEGVKTFALYLYQAKK
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Matches 784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   raffinose. The raffinose synand galactinol efficiently. synthase from cucumber.
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784; Conserv
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30-APR-1998;
04-DEC-1998;
10-DEC-1998;
                                                                                                                                                                                                   New sense raffinose
                                 This sequence represents mustard raffinose synthase, a protein that can bind a D-galactosyl group through an alpha(1-6) bond thydroxy group attached to the carbon atom at the 5-position of D-glucose residue in a sucrose molecule to form raffinose cDN (see AAZ20209) encoding the enzyme was isolated from mustard
                                                                                                                                                                                                                                                                                                                          Watanabe
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                    Juncea)
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in food plants -
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98JP-0120551.
98JP-0345590.
98JP-0351246.
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                    leaf cDNA
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                           VIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVIH
                                                                                                                                                                                                                                                                                                                                                                                                                   VIEGVRHLVDGGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQMPCRLLKFQENYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLESETQIVILEKSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAP-----PSVIKSDAAVNGIDLSGKPLFRLEGSDLLANGHVVLTDVPVNVTVTASPYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAPSFKNGGSNVVSFD----GLNDMSSP-FAIDGSDFTVNGHSFLSDVPENIVASPSPY-
                                                                                                                                              NKFTGVIGAFNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWHSGENPISIEGVKTF
                                                                                                                                                                                                                        DDFWCTDPSGDINGTYWLQGCHMVHCAYNSLWMGNFIQPDWDMFQSTHPCAEFHAASRAI
                                                                                                                                                                                                                                                                                                                                                                                                       VHKGVKCLVDGGCPPGLVLIDDGWQSIGHDSDGIDVEGMSCTVAGEQMPCRLLKFQENFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVVYVHAGDDPFKLVKDAMKVVRVHMNTFKLLEEKTPPGIVDKFGWCTWDAFYLTVNPDG
SAPEGLSSIKYEF
                    SSSGGISVIEYLE
                                                      IQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRACRIDGEDVGFKYDQDQMVVVQVPWPID
                                                                                                                                  NKYTGIIGAFNCQGGGWCRETRRNQCFSQCVNTLTATTNPKDVEWNSGNNPISVENVEEF
                                                                                                                                                                                                                                                                                                                IVRPELSPGLKLTMQDLAVDKIVDTGIGFVSPDMANEFYEGLHSHLQNVGIDGVKVDVIH
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Pred. No. 2.5e-274;
9; Mismatches 114;
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Best Local S
Matches 544
                                                                                                                                                                                                                                                                                                                                                          The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are fully intended to identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequence from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herbicidal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-AUG-2001; 2001WO-EP09892.
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                                            SFDGLN--DMSSPFAIDGSDFTVNGHSFLSDVPENIVASPSPYTSIDKS----PVSVGCF
                                                                                                                                                  -----SDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLHA 178
                                                                                                                                                                                                2002-269010/31
                     KATGPRAGQKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLPEARVIQPVLS
                                                                                                                                      SDSGPGSGSGRPYVLLLPLLEGSFRSSFQSGEDDDVAVCVESGSTEVTGSEFRQIVYVHA
                                                                                                                                                                                                                                 SDSGINGVDFTEKFRLEDSTLLANGQVVLTDVPVNVTLTSSPYL-VDKDGVPLDVSAGSF
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                                                                                                                                                                                    IGFNLDGEPKSHHVASIGKLKNIRFMSIFRFKVWWTTHWVGSNGRDIENETQIIILDQSG
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                                                                                                                                                                                                                                                                                         Similarity
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-DQNDVGMKAFVRDLKDEFSTVDYIYVWHALCGYWGGLRPEAPALPPSTIIRPELS
                                                                                                                                                                                                                                                                                                                                                    herbicides.
                                                                                                                                                                                                                                                                                                                             783 AA;
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Pred. No. 1.9e-269;
9; Mismatches 117;
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30-APR-1998;
04-DEC-1998;
10-DEC-1998;
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                   N-PSDB; AAZ20208
                              WPI; 1999-593144/51.
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                                                  Watanabe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLGRVGDDFWCTD 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVIHLLEMLCE 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIEYLF 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DE--SVEVGVFGAGEFRVYASKKPVSCLIDGEVVEFGY-EDSMVMVQVPW---SGPDGLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKLLLSGLNDDLELTLEPFKFELITVSPVVTIEGNSVRFAPIGLVNMLNTSGAIRSLVYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAFNCQGGGWCRETRRNQCFSECVNTLTATTSPKDVEWNSGSSPISIANVEEFALFLSQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDSVGKHNFDLLKKLYLPDGSILRSEYYALPTRDCLFEDPLHNGETMLKIWNLNKFTGVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSGDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYV 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KYGGRVDLAKAYFKALTSSVNKHFNGNGVIASMEHCNDFMFLGTEAISLGRVGDDFWCTD
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                                                                         SUMITOMO CHEM CO LTD
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98JP-0120551.
98JP-0345590.
98JP-0351246.
                                                                                                                                                   99EP-0107430
                                                                                                                                                                                                                              /note=
348
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LNKFTGVIGAFNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWHSGENPISIEGVKT
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                                                       LNKYNGVLGVFNCQGGGWSRESRKNLCFSEYSKPISCKTSPKDVEWENGHKPFPIKGVEC
                                                                                                             ISGGPIYVSDVVGKHNIPLLKRLVLADGSILRCEYHALPTKDCLEVDPLHDGKTMLKIWN
                                                                                                                                        ISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETMLKIWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
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                                                                                                                                               ID-KSPVS-----VGCFVGFDASEPDSRHVVS1GKLKDIRFMSIFRFKVWWTTHWVGRN
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GHELEHETQMMLLDKNDQLGRPFVLILPILQASFRASLQPGLDDYVDVCMESGSTRVCGS
                                                   GGDLESETQIVILEKSDS-GRPYVFLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDA
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                                                                                                                                                                                                                                                                                                                                              67.6%; Score 2854.5; DB 19; 65.9%; Pred. No. 7.2e-261; tive 123; Mismatches 120;
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                                        WPI; 1999-511112/43
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                                                                                                                          28-NOV-1997;
18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                          Raffinose
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|| |: :|::|:|
WP---SASKLSMVEFLF 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGAIQSMEFDNHIDVVKIGVRGCGEMKVFASEKPVSCKLDGVVVKFDY-EDKMLRVQVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSGAIQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRACRIDGEDVGFKYDQDQMVVVQVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRAISGGPVYVSDCVGKHNFKLLKSLALPDGTILRCQHYALPTRDCLFEDPLHDGKTMLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRVGDDFWCTDPSGDPNGTYWLQGCHMVHCAYNSLWMGNFIQPDWDMFQSTHPCAEFHAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PQAKVYTPKLSNGLKLTMKDLAVDKIVSNGVGLVPPHLAHLLYEGLHSRLESAGIDGVKV
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96JP-0338673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New raffinose synthase gene -
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                                                MAPSI----SKTVELNSFGLVNGNLPLSITLEGSNFLANGHPFLTEVPENIIVTPSP---
WP--
                                                                                                                                                                                                                                                              GRVGDDFWCTDPSGDPNGTYWLQGCHMVHCAYNSLWMGNFIQPDWDMFQSTHPCAEFHAA
                       WPIDSSSGGISVIEYLF
                                                                                                       MNVFAVYLFKDHKLKLMKASEKLEVSLEPFTFELLTVSPVIVLSKKLIQFAPIGLVNMLN
                                                                                                                    VKTFALYLYQAKKLILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPIGLVNMLN: ||:||:| | : : ||||||||||
                                                                                                                                                                        IWNLNKFTGVIGAFNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWHSGENPISIEG
                                                                                                                                                                                                               SRAISGGPVYVSDCVGKHNFKLLKSLALPDGTILRCQHYALPTRDCLFEDPLHDGKTMLK
                                                                                                                                                                                                                           SRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETMLK
                                                                                                                                                                                                                                                                              GRYGDDFWCTDPSGDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAA
                                                                                                                                                                                                                                                                                                                   DVIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISL
                                                                                                                                                                                                                                                                                                                                                                                   PEARVIOPVLSPGLOMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKI 407
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                                                                                                                                                                                                                                                                                                                                                                         POAKVVTPKLSNGLKLTMKDLAVDKIVSNGVGLVPPHLAHLLYEGLHSRLESAGIDGVKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSGVWEGVKGLVEGGCPPGMVLIDDGWQAICHDEDPITDQEGMKRTSAGEQMPCRLVKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PQGVIEGVRHLVDGGCPPGLVLIDDGWQSIGHDSDPIT-KEGMNQTVAGEQMPCRLLKFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFRSMLYLHAGDDPFALVKEAMKIVRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GHELEHETQMMLLDKNDQLGRPFVLILPILQASFRASLQPGLDDYVDVCMESGSTRVCGS
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                                                                                                                                                            IWNLNKYTGVLGLFNCQGGGWCPVTRNKSASEFSQTVTCLASPQDIEWSNGKSPICIKG
                                                                                                                                                                                                                                                                                                                                                                                                                              ENYKFRQYCSGKDS----
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525; Conserv
SASKLSMVEFLF
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Pred. No. 7.2e-261;
3; Mismatches 120;
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RESULT

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AAB49400

ID AAB49400 standard; Protein; 78

XC AAB49400;

XX AAB49400;

XX AAB49400;

XX Soybean raffinose synthase.

XW Plant promoter; transgenic pla

XX Soybean max.

XX Plant promoter; transgenic pla

XX Plant promoter; transgenic pla

XX Clycine max.

XX Plant promoter; transgenic pla

XX Clycine max.

XX Plant promoter; transgenic pla

XX PD 02-NOV-2000.

XX PP 27-APR-2000; 2000EP-0108962.

XX PD 01-SEP-1999; 99JP-0247211.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention provides novel plant promoters which can be used production of transgenic plants which express genes with desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAPSFKNGGSNVVSFD--GLNDMSSPFAI--DGSDFTVNGHSFLSDVPENIVASPSPYTS 56
                                           GHELEHETQMMLLDKNDQLGRPFVLILPILQASFRASLQPGLDDYVDVCMESGSTRVCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAPSI ---- SKTVELNSFGLVNGNLPLSITLEGSNFLANGHPFLTEVPENIIVTPSP--- 53
DVIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISL
                                                                                                                                                                                                                                                                      PQGVIEGVRHLVDGGCPPGLVLIDDGWQSIGHDSDPIT-KEGMNQTVAGEQMPCRLLKFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGDLESETQIVILEKSDS-GRPYVFLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ID-KSPVS-----VGCFVGFDASEPDSRHVVSIGKLKDIRFMSIFRFKVWWTTHWVGRN 109
                                                                                                                                                                                                                                             PSGVWEGVKGLVEGGCPPGMVLIDDGWQAICHDEDPITDQEGMKRTSAGEQMPCRLVKLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDAKSSKNNEDDDVVGCFVGFHADEPRSRHVASLGKLRGIKFMSIFRFKVWWTTHWVGSN 113
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525; Conser
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Pred. No. 7.2e-261;
3; Mismatches 120;
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N-PSDB;
                   The present sequence is a raffinose synthase from clone sfl1.pkl25.d4 isolated from a soybean immature flower cDNA library sfl1. Raffinose synthase is involved in the biosynthesis of raffinose and higher homologues in the raffinose saccharide family from sucrose. The present sequence is useful for reducing the raffinose saccharide content of soybean seeds which improves the nutritional quality of the soy protein products derived from them.
                                                                                                                             Nucleic acids and encoded proteins involved in the biosynthesis raffinose, useful for producing soybean seeds with a reduced racontent and therefore improved nutritional quality - \frac{1}{2}
                                                                                                          Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IWNLNKFTGVIGAFNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWHSGENPISIEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MNVFAVYLFKDHKLKLMKASEKLEVSLEPFTFELLTVSPVIVLSKKLIQFAPIGLVNMLN
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                                                                                                                                              LILSKPSQDL-DIALDPFEFELITVSPVTKLIQTSLHFAPIGLVNMLNTSGAIQSVDYDD
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                protein:
mutein;
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raffinose
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                ID 1.
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synthase;
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N-PSDB; AAH27438.
                                                                                                                                                                                                                                                                                                                                                  Sequence
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The present invention relates to a mutant protein of raffinose synthas in which at least one aromatic amino acid present at the position of about 1-7 amino acids from the N-terminus is deleted or replaced. The mutant protein can be used for reducing the raffinose oligosaccharide content in a plant body. The present protein from soybean, was used in the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GHELEHETQMMLLDKNDQLGRPFVLILPILQASFRASLQPGLDDYVDVCMESGSTRVSGS
SRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETMLK
                                                                              GRVGDDFWCTDPSGDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAA
                                                                                                                                                                                                                                                     PEARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKI 407
                                                                                                                                                                                                                                                                                                                                                        ENYKFRQYCSGKDS-----EKGMGAFVRDLKEQFRSVEQVYV-HALCGYWGGVRPKVPGM
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                                                    GRVGDDFWCTDPSGDPNGTYWLQGCHMVHCAYNSLWMGNFTQPDWDMFQSTHPCAEFHAA
                                                                                                                                                       DVIHLLEMLSEEYGGRVELAKAYYKALTASVKKHFKGNGVIASMEHCNDFFLLGTEAIAL
                                                                                                                                                                                                   DVIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISL
                                                                                                                                                                                                                                                                                                                                                                                     ENYKFRDYVNPKATGPRAGQKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2834; DB 22;
Pred. No. 6.3e-259;
Pl; Mismatches 120;
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                                 Query Match
Best Local S
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                                                                                                 This sequence represents the broad bean raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosy1 group through an alpha (1-6) bond with a hydroxy1 group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides in the host organism or cell is changed. Raffinose oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
                                                                              Sequence
                                                                                                                                                                                                                Claim 1; Page
                                                                                                                                                                                                                                     New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                     Oeda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raffinose synthetase; metabolism modification; gastrointestinal flora; broad bean.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MNVFAVYLFKDHKLKLMKASEKLEVSLEPFTFELLTVSPVIVLSKKLIQFAPIGLVNMLN
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                                             Similarity
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                                Score 2767; DB 19;
Pred. No. 1.5e-252;
8; Mismatches 140;
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                                   JP11215984-A
                                                                            Raffinose synthase;
                                                                                                   Amino acid
                                                                                                                         26-OCT-1999
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                                                                                                                                                                                                                                                                                   AIQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRACRIDGEDVGFKYDQDQMVVVQVPWPI 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVI
||:|:|:||:||:|||:|||:|||:|||
RVVVPKVSQGLKMTMEDLAVDKIVENGVGLVPPDFAHEMFDGLHSHLESAGIDGVKVDVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVISTIDIGNGNSPLFSITLDQSRDFLANGHPFLTQVPPNITTTTTTTASSFLNLKSNKD
                                                                                                                                                                                                                                                                                                                                FALYLYQAKKLILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPIGLVNMLNTSG
                                                                                                                                                                                                                                                                                                                                                                            LNKFTGVIGAFNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWHSGENPISIEGVKT
                                                                                                                                                                                                                                                                                                                                                                                                         ISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETMLKIWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVWEGVKSLTDGGCPPGFVIIDDGWQSICHDDDDEDDSGMNRTSAGEQMPCRLVKYEENS
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                                                                                                                                                                                                                                                 DSSSGGISVIEYLF 784
                                                                                                                                                                                                                                                                       AIQSLEEDDNASLVKIGVRGCGEMSVFASEKPVCCKIDGVKVKFLY-EDKMARVQILWP-
                                                                                                                                                                                                                                                                                                                    FAVYFFKEKKLRLMKCSDRLKVSLEPFSFELMTVSPVKVFSKRFIQFAPIGLVNMLNSGG
                                                                                                                                                                                                                                                                                                                                                                LNKYTGVLGLFNCQGGGWCPEARRNKSVSEFSRAVTCYASPEDIEWCNGKTPMSTKGVDF
                                                                                                                                                                     standard;
                                                                                                  sequence of a raffinose synthase protein.
                                                                                                                        (first entry)
                                                                                                                                                                      Protein;
                                                                             plant;
                                                                              broad bean;
                                                                              sucrose; raffinose.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New raffinose synthase gene - is prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-NOV-1997;
18-DEC-1996;
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                                                                           LNKFTGVIGAFNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWHSGENPISIEGVKT
                                                                                                                                                                                                   GDDFWCTDPSGDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAASRA
                                                                                                                                                                                                                                                               HLLEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLGRV
                                                                                                                                                                                                                                                                                                         RVVVPKVSQGLKMTMEDLAVDKIVENGVGLVPPDFAHEMFDGLHSHLESAGIDGVKVDVI
                                                                                                                                                                                                                                                                                                                     RVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVI 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSMLYLHAGDDPFALVKEAMKIVRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVHPQ 230
                              FALYLYQAKKLILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLHFAPIGLVNMLNTSG
                                                                                                                                                    ISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETMLKIWN 590
                                                                                                                                                                                  GDDFWCSDPSGDPNGTYWLQGCHMVHCAYNSLWMGNFIQPDWDMFQSTHPCAEFHAASRA
                                                                                                                                                                                                                                              HLLELLSEEYGGRVELARAYYKALTSSVKKHFKGNGVIASMEHCNDFFLLGTEAISLGRV
                                                                                                                                                                                                                                                                                                                                                                 KFREYENPE----NGGKKGLGGFVRDLKEEFGSVESVYVWHALCGYWGGVRPGVHGMPKA
                                                                                                                                                                                                                                                                                                                                                                                               KFRDYVNPKATGPRAGQKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLPEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVISTIDIGNGNSPLFSITLDQSRDFLANGHPFLTQVPPNITTTTTTTASSFLNLKSNKD
FAVYFFKEKKLRLMKCSDRLKVSLEPFSFELMTVSPVKVFSKRFIQFAPIGLVNMLNSGG
                                                            LNKYTGVLGLFNCQGGGWCPEARRNKSVSEFSRAVTCYASPEDIEWCNGKTPMSTKGVDF
                                                                                                                        ISGGPIYVSDCVGNHNFKLLKSLVLPDGSILRCQHYALPTRDCLFEDPLHNGKTMLKIWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KACLYIHLSNDPYSILKEAVKVIQTQLGTFKTLEEKTAPSIIDKFGWCTWDAFYLKVHPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 19-21; 40pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - VSVGCFVGFDASEPDSRHVVSIGKLKDIRFMSIFRFKVWWTTHWVGRNGG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97JP-0329006.
96JP-0338673.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2767; DB 20; Pred. No. 1.5e-252;
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RESULT 13
AAW57888
ID AAW57
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                                                                                                                                                               Best Local Similarity
Matches 448; Conser
                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                         This sequence is the Japanese artichoke raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides in the host organism or cell is changed. Raffinose oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Raffinose synthetase; metabolism modification; gastrointestinal flora; Japanese artichoke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
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121
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                                                                     SFRSMLYLHAGDDPFALVKEAMKIVRTHLGTERLLEEKTPPGIVDKFGWCTWDAFYLTVH 228
                                                                                                                                     NGGDLESETQIVILEKSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDA 168
                                                                                                           NGSDLERETQIVVLDKSDD-RPYIVLLPLIEGQFRASLQPGVDDFIDICVESGSTKVNES
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PHGVMEGVQGLVDGGCPPGLVLIDDGWQSICHDNDALTTEGMGRTSAGEQMPCRLIKFEE
                                                     SFRASLYMHAGDDPFTLVKDAVKVARHHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLNVQ
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Pred. No. 3.2e-
62; Mismatches
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                                                                                                                                                           e 2529; Up _
i. No. 3.2e-230;
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                                                                                                                                                                                            587;
                                                                                                                                                                                                                                                                                                                                         e of the raffinose by
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Query Match
Best Local
                          Matches
                                                                            Sequence
                                                                                                 The present sequence represents a raffinose synthase protein. sequence is isolated from plant material. The protein forms resequence is isolated from blant material. The protein forms reby complexing alpha(1 to 6). D-galactosyl hydroxyl group of the D-galactosyl sequence of D-galactosyl sequence.
                                                                                                                                                                  Claim 12;
                                                                                                                                                                                       New raffinose synthase gene - is prepared
                                                                                                                                                                                                                 N-PSDB; AAZ10003
                                                                                                                                                                                                                               WPI; 1999-511112/43.
                                                                                                                                                                                                                                                                                28-NOV-1997;
18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                               10-AUG-1999.
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                                                                                                                                                                                                                                                                                                                                                                                             Stachys sieboldii
                                                                                                                                                                                                                                                                                                                                                                                                                      Raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a raffinose synthase protein.
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109 NGGDLESETQIVILEKSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCVESGSSKVVDA 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIHLLEMLCEDYGGRVDLAKAYYKALSSSYNNHFNGNGVIAGLEHCNDFMFLGTEAITLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WNLNKFTGVIGAFNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWHSGENPISIEGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLG 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NYKFRDYVNPKATGPRAGQKGMKAFIDELKGEFKTVEHVYVMHALCGYWGGLRPQVPGLP 348
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                          al Similarity
448; Conserv
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                                                                            587 AA;
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                       Score 2529; DB 20;
Pred. No. 3.2e-230;
2; Mismatches 70;
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Misc-difference 132
                                                                                                                                                               Misc-difference 143
                                                                                                                                                                                                                                                     Brassica napus
 30-APR-1998;
                                                  03-NOV-1999
                                                                           EP953643-A2
                                                                                                              Misc-difference
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                                                                                                                                                                                                                 Misc-difference
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                          27-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PQGVIEGVRHLVDGGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQMPCRLLKFQE 288
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                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                             /note=
148
 98JP-0120550
                          99EP-0107430
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                                                                                                    /note=
                                                                                                                                                   /note=
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                                                                                                                                                                                                                                                                                                                                                                                 Protein;
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                                                                                                                                                  "encoded by
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04-DEC-1998;
10-DEC-1998;
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KRVTSKTNPKDIEWHSGENPISIEGVKTFALYLYQAKKLILSKPSQDLDIALDPFEFELI
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Search completed: April 4, 2003, 11:11:09 Job time: 80 secs

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LON_CAMJE
AGA1_PEDPE
AGA1_PAT
CARB_THETN
IMA1_XERMA
CHIA_SERMA
PULA_THEMA
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HMCS_RAT
ENV_EIAV2
TAGA_VIBCH
POLG_PVYHU
YIHI_YEAST
DHMI_PARDE
HMCS_HUMAN
HEMA_IAGRE
RRPO_MCMY
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003745 bacillus th 0944k1 homo sapien P45177 haemophilus p19700 influenza a 000330 salmonella 000156 ictalurid h P51617 homo sapien P55031 synechocyst 009435 caenorhabdi P42242 bacillus su p13217 drosophila p13704 cricetulus p13217 genome p0 p40512 saccharomyc p22428 equine influenza p1698 influenza p1698 influenza p1698 influenza p1698 influenza p1698 influenza p11640 maize chlor 09a368 caulobauter 09a576 rhizobium m069300 campylobact p43467 pediococcus 001728 rattus morvoga salado thermoanaer 09a3840 thermoanaer 09a3840 thermoanaer 09a3840 thermoanaer
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EMBL; AL031324; CAA20445.1;		or send an email to license@isb-sib.ch).	entities requires a license agreement (See http://www.isb-sib.ch/announce/	use by non-profit institutions as long as its content is in no way	European Bioinformatics Institute. There are no restrictions on	between the Swiss Institute of Bioinformatics and the EMBL outstation -	This SWISS-PROT entry is copyright. It is produced through a collaboration		-!- SIMILARITY: CONTAINS 11 WD REPEATS (TRP-ASP DOMAINS).	Nature 415:871-880(2002).	"The genome sequence of Schizosaccharomyces pombe.";	Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;	Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,	Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,	Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,	Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,	Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,	Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,	Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,	BORZYM K. Langer I. Beck A. Lehrach H. Reinhardt R. Pohl T.M.	Weirlens in vanstreets in Rieger M., Schaeter M., Mueiter S., Gabel O. Bishors H. Golder M., Mueiter Sudanter M.,	WOULHWALL I., VOICEAGEL G., MELL N., NOUDBEL J., VINCHPLES D.,	Taylor K., Taylor K.G., Tivey A., Walsh S.V., Walfen T., Whitehead S.,	Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,	Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,	Tambas K. Tonbas I. Tonbas M. Loathber S. McConald S. McCoan I.	A Gentles S., Gobie A., Hamilin N., Harits D., Hidalyo J., Hodgson G.,	COLLINS M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,	Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,	Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,	MEDI-TUE-21848401: DITMOG-11859350:	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=4896;	Schizosaccharomyces.	Schizosaccharomycetales: Schizosaccharomycetaceae:	Schizosaccharomyces pombe (Fission yeast).		l WD-repea	(Rel. 30,	15-JUL-1998 (Rel. 36, Created)	Cremonico, Ext.	ULT 1 7_SCHPO CTANDADD. DDT. 000	

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InterPro; IPR001680; WD40

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PROSITE; PS50082; WD_REPEATS_2; 2.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
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RLDD-
                                                                                                                                               KPVTAVMLDNVNRILVTASLDGILKFWDFNKGNLIDSLDVGSSITHAIYQHSSDLVAVAC
                                                                                                                                                                                               QHVLPTSDGTSVRSVCVSCCGNFGLIGSSKGVVDVYNMQSG-----IKRKSFGQSSLSG
                                                                                                                                                                                                                                                                    DGSIL-----RSEYYALP-----TRDCLFEDPL--HNGETMLKIWNLNKFT--
                                                                                                                                                                                                                                                                                                                                                                      D-DFWCTDPSGDPNGTF------WLQGCHMVHCA--NDSL--WM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                               NTNADITSLLHPSTYLNKILLGFSDGALQIWNLRVSKRVHEFQEFFG-DGITSLTQAPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVEQEHGTVTHLDAFGEWIIACTSSRHVYVWKHASKY-----SVPE---LHTTFLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELKGEFKTV-----EHVYVWHALCGYWGGLRPQVPGLPEARVIQPVLSP 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVGNTFQTYDCEKLNLLFVGKQLDKEITCLK---SFKDFMLVAAGSKIFAYKRGKIIWDI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGHDSDPITKEGMNQTVAGEQMPCRLLKFQENYKFRDYVNPKATGPRAGQKGMKAFID- 315
                       RIDGEDVGFKYDQDQMVVVQVPWPIDSSSGGISVIE
                                                                      ----TSLHFAPIGLVNMLNTSGAIQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRAC
                                                                                              DDFGIRIVDVQTRKIVRELWGHSNRLTSFDFSDTGRWLVTASLDGTIRTWDLPTGHLIDS
                                                                                                                                                                       KRVTS----KTNP-----
                                                                                                                                                                                                                                               QGSVISKAKKLNVRPEELKLPEITALSSSNTREKYWDNVLTAHKNDSSARTWNWKSKTLG
                                                                                                                                                                                                                                                                                              RSRNGHYEPPSFVKFYGKSVHFLISAATDRSLRAVS---LY-QDS
                                                                                                                                                                                                                                                                                                                        ----GNFIHPDWDMF--QSTH--PCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLVLP
                                                                                                                                                                                                                                                                                                                                               DLSFWDLSKRRIQNVTYNAHFGSLPKIQFLNGQPILVTAGPDNSLKEWIFDSMDGAPRIL
                                                                                                                                                                                                                                                                                                                                                                                              DVLAVGTISGRI----VIFNLKNGSILMEFKQDGQVLSCSFRTD----GTPILASSNPIG
                                                                                                                                                                                                                                                                                                                                                                                                                      EMLC-EDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAI-SLGRVG 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLQMTMEDLAVDKIVLHKVGLVPPEKAEEMY-----EGLHAHLEKVGIDGV-KIDVIHLL 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
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437
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611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100569 MW;
-VVEVSAPSVSGEKGISVVE 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat;
                                              <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 115.5; E
Pred. No. 0.35;
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                                                                                                                                                                       KDIEWHSGENPISIEGVKTFALYLYQAKKLILSKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WD repeat.
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D 2.
D 3.
D 4.
D 5.
D 6.
D 7.
D 8.
D 9.
D 10.
D 11.
SEEFFC6034BDC047 C
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                                                                                                                                                                                                                      -GVIGAFNCQGGGWCRETRRNQCFSQYS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      902;
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                                                                                                                                                                                                                                                                                                                                                                                              268
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cleb_BACTA STANDARD; PRT; 1174 AA. 003745; 003745; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Pesticidial crystal protein cryleb (Insecticidal Cryleb)) (Crystaline entomocidal protoxin) (134 CRYLEB OR CRYLE(B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001178; Endotoxin.
Pfam; PF00555; endotoxin; 1.
Toxin; Sporulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. The There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genes encoding lepidopteran-active toxins and transformed Patent number US5206166, 27-APR-1993.
-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Toxin; Sporulation SEQUENCE 1174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAE.
-!- DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=NRRL B-18457 ,
Payne J.M., Sick A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus thuringiensis (subsp. aizawai)
Bacteria; Firmicutes; Bacillales; Bacil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M73253; AAA22346.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF THE SPORE COAT.
-!- MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P02965; 1CIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1433;
                 809
                                                                                                                                                                                        486
                                                                                                                                                                                                                                                          426
                                                                                                                     546
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                                                                                                                                                                                                                          469
                                                                                                                                                                                                                                                                                                                                                                                                                               336 YWGGLR------PQVPGLPE-----ARVIQPVLSPGLQMTMEDLA-----VDK 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-TERMINUS.
WCRETRRNQCFS-QYSKRVTSKTN--
                                                                                                                                                                                                                                                                                                                                                                                              YWAGHRVTSHFTGSSQVISSPQYGITANAEPSRTIAPSTFPGLNLFYRTLSDPFFRRSDN 373
                                                                                                                                                                                        FTGGDIIRTNVNGNVLSMSLNFSNTSLQRYRVRVRYAASQTMVMRVNVGGSTTFDQGFPS
                                                                                                                                                                                                                                                                                          GRVDLAKAYYKAMTKSI ---
                                                                                                                                                                                                                                                                                                                                                            I------VLHKVGLVPPEKAEEMY--EGLHAHLEKVGIDGVK--IDVIHLLEMLCEDYG
                                                                                                                   TMSANGSLTSQSFRFAEFPVGIST---
                                                                                                                                                       VHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLV
                                                                                                                                                                                                                                                        SHYTLTRSLYNTNITSLPTFVWTHHSATDRNITYPDVITQIPLVKSFSLTSGTSVVRGPG
                                                                                                                                                                                                                                                                                                                            IMPTLGINVVQGVGFIQPNNGEVLYRRRGTVDSLDELPIDGENSLVGYSHRL------
                                                 IPVDATFEAEYDLERAQKAVNSLFTS---SNQIELKTDVTDYHIDQVSNLV---DCLSDE
                                                                                   LPDGSILRSEY - - - YALPTRDCLFEDPLHNGETMLKI - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.5%;
19.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133601 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 107;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                        -NKHFKGNGVIASMEHCNDF-MFLGTEAI-SLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5EEA0BA7FD63480F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillaceae;
                                                                                                                     -SGSQTAG-ISISNNPGRQTFHLDRIEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181;
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                                                                                                                                                                                                                          ----PNGTFWLQGCHM
                 --PKDIEWHSG----
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AND AS F
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AIM1_HUMAN
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                                                                                                                                                                                                     InterPro; IPR001064; Crystallin.
InterPro; IPR000772; Ricin_B_lectin.
Pfam; PF00030; crystall; 6.
Pfam; PF00652; Ricin_B_lectin; 3.
PRINTS; PR01367; BGCRYSTALLIN.
SMART; SM0045B; RICIN; 1.
SMART; SM00247; XTALD9; 6.
PROSITE; PS00221; RICIN_B_LECTIN; 1.
PROSITE; PS00231; RICIN_B_LECTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U83116;
EMBL; U83115;
HSSP; P02526;
                     DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 superfamily, is associated with the control of tumorigenicity mallgnant melanoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Absent in melanoma 1 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 601797; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:356; AIM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97250519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAY M.E., Wistow G., Su Y.A., Meltzer P.S., Trent J.M.;
"AIM1, a novel non-lens member of the betagamma-crystallin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C. Natl. Acad. Sci. U.S.A. 94:3229-3234(1997).

FUNCTION: MAY FUNCTION AS SUPPRESSOR OF MALICANANT MELANOMA. I FUNCTION: THROUGH INTERACTIONS WITH THE CYTOSKELETON. SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY. CONT 6 TANDEM REPEATS OF A BETA/GAMMA-TYPE CRYSTALLIN DOMAIN.

SIMILARITY: CONTAINS 1 RICIN B-TYPE LECTIN DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V-GCTDLQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDRGWRGSTDITIQGGDDVFKEN
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                           Lectin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1GAM
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                     CRYSTALLIN BETA/GAMMA-LIKE 1
CRYSTALLIN BETA/GAMMA-LIKE 2
CRYSTALLIN BETA/GAMMA-LIKE 3
CRYSTALLIN BETA/GAMMA-LIKE 4
CRYSTALLIN BETA/GAMMA-LIKE 5
CRYSTALLIN BETA/GAMMA-LIKE 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISFSGMS-LSDTMTLRGS-------VQNKLNPRPGKVVIYSEPDVSEKCIEVFSD 1042
KSDG--RIYSKLKPNLVLDIKG---GTQYDQNHIIL 1704
                                                                                                                                                            YSKRVTSKTNPKDIEWHSGENPISIEGVKTF - -
                                                                                                                                                                                                                          GVIGAFNCQ------GGGW------
                                                                                                                                                                                                                                                          SAMGCPPGATFKS----LRFIDVEFSEPTIILFEREDFKGKKIELNAETV----NLRSL-
                                                                                                                                                                                                                                                                                                                      QFQGHS-----QSFEETTSQIDDSFSTKSCRVSGGSWVVYDGENFTGNQYVLEEGHYPCL
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                               KGCGEMRVFASKKPR-ACRIDGEDVGFKYDQDQMVV 763
                                                                                            DLDIALDPFEFELITVSPVTKLIQTSLHFAPIGLVNMLNTSGAIQSVDYDDDLSSVEIGV
                                                                                                                            --KRIYFRLRNKATGLFMSTNG-NLEDLKLLRIQVMEDVGADDQIWIYQ-EGCIKCRIAE
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                                                                                                                                                                                                                                                                                                                                                                                                                      FKGNGVIASMEHCNDFMFLGTEAISLGRVGDDFWCTDPSGDPNGTFWLQGCHMVHCANDS
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7; Mismatches
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Pred. No. 5
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                                                                                                                                                            ---ALYLYQAKKLILSKPSQ
                                                                                                                                                                                                                          ------CRETRRNQCFSQ
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Pfam;
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MEDLINE-95350630; PubMed-7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitchugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Heblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLycogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U32815; TIGR; HI1357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 269:496-512(1995).
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Bacteria; Proteobacteria;
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1,4-alpha-glucan
        289
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InterPro; IPR004193; Isoamylase_N.
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SIMILARITY: BELONGS TO FAMILY 13 OF
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NYKFRDYVNPKATGPRAGQKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLP
                                                                                                                                                                                                         AGDDPFALVKEAMKIVRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVHPQGVIEGVR
                                                                                                                                                         QGNQP-----ISIYEVHLGSWR-----RNLENNF-WLDYDQIADELIPYVKEMGFT
                                                                                                                                                                                                                                                            ASLGQLYKFELIDCHGNLRLKADPFAFSSQLRPDTASQVSALPNVVEMTEARKKA---
                                                                                                                                                                                                                                                                                                                                                                                                                VGFDASEPDSRHVVSIGKLKDIRFMSIFRFKVWWTTHWVGRNGG---DLESETQIVILEK 124
                                                                                                                                                                                                                                                                                                               SDSGRPYVFLLPIVEG-----PFRTSIQPGDDDFVDVCVESGSSKVVDASFRSMLYLH
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117; Conserv
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PF02922; isoamylase_N;
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                                                                                                   -VDGGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQMPCRLLKFQE
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                                                                                   Envelope
SIGNAL
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01-FEB-1991 (R
01-FEB-1991 (R
16-OCT-2001 (R
Hemagglutinin
                                                                                                                                                                                                                 MEDLINE-89204912; PubMed-2705304;
Donis R.O., Bean W.J., Kawaoka Y., Webster R.G.;
"Distinct lineages of influenza virus H4 hemagglutinin genes in different regions of the world.";
Virology 169:408-417(1989).
-I- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS CELL RECEPTORS AND FOR INITIATING INFECTION.
                                                                                                                    InterPro; IPR001364; Hemagglutn.
Pfam; PF00509; Hemagglutinin; 1.
PRINTS; PR00329; HEMAGGLUTN12.
             CARBOHYD
                                                             CHAIN
                                                                          CHAIN
                                                                                                            ProDom;
                                                                                                                                                            HSSP;
                                                                                                                                                                                 -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS (HA1 AND HA2) LINKED BY A DISULFIDE BOND. -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAC
                                                                                                                                                                                                                                                                                                                                        Influenza A virus (strain A/Ruddy Turnstone/New Jersey/47/85). Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses; Influenzavirus A.
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                                                                                                                                                                                                                                                                                                                                                                Influenza
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                                                                                                                                                          G34214; HMIVF7.
; P03437; 2VIU.
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                                                                                                            PD000225;
                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 17, Created)
(Rel. 17, Last sequence update)
(Rel. 40, Last annotation updat
in precursor [Contains: Hemagglu
in HA2 chain].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       630
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                                                                                              Hemagglutinin;
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                                                           HEMAGGLUTININ
                                                                       HEMAGGLUTININ
                                                                                             Glycoprotein;
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Hemagglutinin
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(GLCNAC.)
(GLCNAC.)
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 (GLCNAC
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(POTENTIAL).
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O00310;

O1-OCT-1994 (Rel. 30, Created)

O1-OCT-1994 (Rel. 30, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                         MEDLINE=92349966; PubMed=1379320;
Brown P.K., Romana L.K., Reeves P.R.;
"Molecular analysis of the rfb gene cluster
muenchen (strain_M67): the genetic basis of
                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella cholerae-suis (Salmonella enterica)
Bacteria; Proteobacteria; gamma subdivision; E
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                     MICROBIOI. 6:1385-1394(1992).
FUNCTION: INVOLVED IN GDP-MANNOSE BIOSYNTHESIS WHICH SERVES AS THE ACTIVATED SUGAR NUCLEOTIDE PRECURSOR FOR MANNOSE RESIDUES IN CELL SURFACE POLYSACCHARIDES. THIS ENZYME PARTICIPATES IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LANNGKF-EFIAEEFQWNTVKQNGKSGACKRANVNDFFR-RLNWLTKSDGNAYPLQNLTK 181
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Matches 59
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Pfam; PF02880;
PROSITE; PS0071
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Q00156;
Q1-DEC-1992
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PIR; S22622; S22622
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-1- PATHWAY: GDP-MANNOSE BIOSYNTHESIS WITHIN THE O ANTIGEN

BIOSYNTHESIS PATHWAY OF LIPOPOLYSACCHARIDE BIOSYNTHESIS.

-1- SIMILARITY: BELONGS TO THE PHOSPHOHEXOSE MUTASES FAMILY.
Davison A.J. "Channel cat
                                                                                                       SEQUENCE FROM N.A. STRAIN-Auburn 1;
                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical
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                                                                          MEDLINE=92087490;
                                                                                                                                                                                                               NCBI_TaxID=10401;
                                                                                                                                                                                                                                                                                                                   Ictalurid herpesvirus 1 (Channel catfish virus) (CCV).
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59; Conser
   catfish
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PGM_PMM_III; 1.
10; PGM_PMM; 1.
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. 24, Last sequence up.
. 24, Last annotation of the control of th
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FORMS THE PHOSPHOSERINE INTERMEDIATE
(BY SIMILARITY).

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Best Local Similarity
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                                                                                                                                                                                                                        IRA1_HUMAN
P51617;
                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Interleukin-1 receptor-associated kinase 1 (EC
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE FROM N.A., AND PARTIAL SMEDLINE=96180673; PubMed=8599092. Cao Z., Henzel W.J., Gao X.;
                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                           _HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein SEQUENCE 514 AA;
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                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                         TELFWVIANI -- CT-FIFIHNKTIKLHH-GD---APDLNIDELPDGLYLFNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QPVLSPGL------QMTMEDLAVDKIVLHKV-----GLVPPEKAEEMYEGLHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFRTSIQPGDDDFVDVCV-ESGSS-KVVDASFRSMLYLH-----AGDDP-----FAL
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                                                                                                                                                                                                                                                                                                                                                                                                                         -----HLEKVGI--DGV-----KIDVIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKH 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -QLIDSNFCVLCMYESDHSLATADTRFKTILCDHFTEASVTAGGDPCDSAEVTAV
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                                                                                                                                                                                                                                         STANDARD;
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                                                                                  Chordata;
Primates;
                               AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 101; DB Pred. No. 2.3;
                                                                                  Craniata; Vertebrata; Euteleostomi Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88E7302A1424D29C CRC64;
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                                                                                                                                                     2.7.1.-) (IRAK-1).
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Best Local
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted -!- FUNCTI
                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00069; pkinase; Pfam; PF00531; death; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U52112; AAC51752.1; -.
EMBL; AF030876; AAC08756.1; -.
EMBL; AF031075; AAF21636.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L76191; AAC41949.1; EMBL; U52112; AAC51752.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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[2]
                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                            Transferase;
                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD000001; PROSITE; PS00107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:6112; IRAK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- PTM: AN EXTENSIVE PHOSPHORYLATION OF ASSOCIATION WITH IL1-R-1. THIS STEP (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-1995) to the
                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
 289
                                                       235
                                                                                   174
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                                                                                                                                           116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEPENDENT: TISSUE SPECIFICITY: SEEMS TO BE UBIQUITOUS, ALTHOUGH PRESENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chwald K., Kloschis P., Rosenthal A., Platzer M.;
mitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
FUNCTION: INVOLVED IN IL-1 PATHWAY. THIS KIMASE ASSOCIATES WITH
THE IL-1 RECEPTOR IL1-R-1. THIS ASSOCIATION IS RAPID AND IL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVATION OF THE KINASE.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMALL AMOUNTS
                                                                                   LYL-----HAGDDPFALVKEAMKIVRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVH 228
                                                                                                                                        ETQIVILEKSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCV--ESGSSKVVDASFRSM 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300283;
GFLPNGSLEDRLHCQTQACPP
                          ---PQGVIEGVRHLVDGGCPP 246
                                                                                                             ESSYSLLQ----GARPFPFCWPLCE-----ISRGTHNFSEELKIGEGGFGCVYRAVMRNT
                                                                                                                                                                                                                                                                                                                                      PS00108;
                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      IPR000719; Euk_pkinase.
IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000488; Death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBFAMILY.
                                                                                                                                                                                                                             712
                                                                                                                                                                                                                                       212 521 PROTEIN KINASE; ATP-binding.
212 521 PROTEIN KINASE.
218 226 ATP (BY SIMILARITY).
229 ATP (BY SIMILARITY).
239 338 BY SIMILARITY.
196 196 F -> S (IN REF. 1).
532 532 S -> L (IN REF. 1).
                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                     PROTEIN_KINASE_ATP; 1
PROTEIN_KINASE_ST; 1.
PROTEIN_KINASE_DOM; 1
                                                                                                                                                                                                                                                                                                                                                                              Euk_pkinase;
                                                                                                                                                                                                                           76536 MW;
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27.08;
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                                                                                                                                                                                  Score 100.5;
Pred. No. 4.1;
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COULD
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BE LINKED TO
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RESULT 9
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01-OCT-1996
01-OCT-1996
16-OCT-2001
                                                                                                                                                                                                                METAL
SEQUENCE
                                                                                                                                                                                                                                                           NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-115(1996).

-I- CATALYTIC ACTIVITY: 2 L-glutamate + 2 oxidized ferredoxin = L-glutamine + 2-oxoglutarate + 2 reduced ferredoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimu Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A Yamada M., Yasuda M., Tabata S.;
"Sequence analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95244836; PubMed-7727752;
Navarro F., Chavez S., Candau P., Florencio F.J.;
"Existence of two ferredoxin-glutamate synthases in terminate the synthases of two ferredoxins sp. PCC 6803. Isolation inactivation of gitB and gitS genes.";
Plant Mol. Biol. 27:753-767(1995).
                                                                                                                                                                                                                                                                                                                                   Pfam; PF01493; DUF14; 1.
Pfam; PF01645; Glu_synthase;
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X80485; CAA56652.1; -. EMBL; D90902; BAA17018.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR002932; Glu_synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ÷
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   218
                                 452
                                                             176
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                                                                                                                      120 VILEKSDSGRPYVFLLPIVEGPFRTS----IQPGDDDFVDVCVESGSSKVVDASFRSMLY 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: TO OTHER GLUTAMATE SYNTHASES. CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-21 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATHWAY: GLUTAMINE SYNTHETASE/GOGAT PATHWAY IN THE ASSIMILATION OF AMMONIA. SYNTHASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: 2 L-glutamate + 2 oxidized fer glutamine + 2-oxoglutarate + 2 reduced ferredoxin. COFACTOR: BINDS A 3FE-4S CLUSTER; FAD AND FMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OR SLL1502.
CTWDAFYLTVHPQGVIEGVRHLVDGGCPPGLVLIDDG
                                                                                        LVIMASEAG - - - - VLPI - - EPERVAKKGRLQPGRMFLVD - - MEQGRI - IADEEIK - - - -
                                                            LHAGDDPFALVKEAMKIVRTH------KGTFRLLEEKTPPGIVD------KFGW
                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyanobacteria;
                                                                                                                                                                                                                                                                                                       biosynthesis;
                                                                                                                                                                                                                1097
1150
1156
1161
1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel.
                                                                                                                                                    Conservative
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                                                                                                                                                                                                                ξ.
                                                                                                                                                                                                                                                                                                                     Iron-sulfur;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34,
40,
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1161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (strain
                               -QEIVSQHPYGEWLAANLKSLEQLPSPGNVPGTDAESLRQRQMAFGY
                                                                                                                                                                 19.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glutamate synthase 1 (EC
                                                                                                                                                                                                                169071
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                                                                                                                                                                                                                                                                                                       lfur; 3Fe-4S; Flavoprotein; FAD;
Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCC 6803)
                                                                                                                                                    , 68
                                                                                                                                                                                                  FMN (BY SIMILARITY).
FMN (BY SIMILARITY).
IRON-SULFUR (3FE-4S) (BY SIMILARITY).
IRON-SULFUR (3FE-4S) (BY SIMILARITY).
IRON-SULFUR (3FE-4S) (BY SIMILARITY).
                                                                                                                                                  Score 100; DB
Pred. No. 14;
99; Mismatches
                                                                                                                                                                                                                                                                                       GLUTAMINE AMIDOTRANSFERASE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synechocystis
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                                                                                                                                                    224;
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                                                                                                                                                                               Length 1550;
                                                                                                                                                    Indels
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RESULT
GLGB_SY
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01-OCT-1996 (Rel. 3
01-OCT-1996 (Rel. 3
15-JUN-2002 (Rel. 4
                                                                                                                                                                       Sugiura M., Tabata S.;
Sugiura M., Tabata S.;
"Sequence analysis of the genome of the unicellular cya
"Sequence analysis of the genome features
Synechocystis sp. strain PCC6803. I. Sequence features
Synechocystis sp. strain PCC6803. I. Sequence features
Synechocystis sp. strain PCC6803. I. Sequence features
                                                                                                                                                                                                                                                                                                                                             enzyme)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLCB_
                                              This
                                                                                                                                                                                                                                                                                               Synechocystis sp. (strain Bacteria; Cyanobacteria; Cyanobacteria; CRBI_TaxID=1148;
                                                                                                                                                               region from map positions 64\% to DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A MEDLINE-96127529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYNY3
                               between
                                                                                                                                                                                                                                       Kaneko T., Tanaka
                                                                                                                                                                                                                                                                                                                                                                         1,4-alpha-glucan branching
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266
                                                                                   PATHWAY: Glycogen biosynthesis; third step. SUBUNIT: MONOMER (BY SIMILARITY). SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL
                 European
                                                                          KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                 CATALYTIC ACTIVITY:
             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --LYLYQAKKLIL----SKPSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRSEYYAL------PTRDCL-FED----PLHNGETMLKIWNLNKF-TGVIGAFNCQG
                                                                                                                                                                                                                                                                                                                                               OR SLL0158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSLYLSQAKEIQIKMAQGAKPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGWCRETRRNQCFSQYSKRVTSKTN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFMFLGTEAISLGR-VGDDFWCTDPSGDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLEKVGIDGVKIDVIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEHCN 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FDPNQGEAGLKTALDNLFTEADQAISQGANLIILSDRQVSAEKAAI-PALLAVSGLHHHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYNY3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSTSKEAHESLATAM - - NRIGGKSNTGEGGEDPERFTWTNDQGDSKNSATKQVASGRFGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYKQYAALVNEQNQKFFTLRGLLDFQDRESIPLEEVEPIEAI - - MKRFKTGAMSY - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FQSTHPCAAFHAASRAISGGPIYVSDSVGKHNF-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRNGSRTKV-GL-----VLESGEPREVHHFAV--LLGYGCGAINPYLAFETLDGMIA
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non-profit
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34, Last
41, Last
                                                                                                                                                                                                                                  PubMed=8590279;
A., Sato S., Kotani H.,
                                                                                                                                                                                                                                                                                                                               (strain
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                                                                                                                                              Formation of 1,6-glucosidic
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2.4.1.18) (Glycogen branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IQGSDLGVIAQEAILR--
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                                                                                        HYDROLASES,
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DOMAIN OF PROTEIN KINASES
-!- SIMILARITY: BELONGS TO ADI

BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL

CONSERVED REGION

OF

CATALYTIC

CYCLASE

-!- SIMILARITY: SOME SIMILARITY WITH

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Best Local :
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Glycogen
                                                                                                                                                      01-NOV-1995 (Rel.
01-NOV-1995 (Rel.
16-OCT-2001 (Rel.
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
                                                                                              Eukaryota; Metazoa; Nemata
Rhabditidae; Peloderinae;
                                                                                                                      Caenorhabditis elegans
                                                                                                                                  Guanylate cyclase receptor-type GCY-1 OR AH6.1.
                                                                                                                                                                                           Q09435;
                                                                                                                                                                                                      CYG1_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete ACT_SITE
                                      Jassal B
                                                 STRAIN-Bristol
                                                             SEQUENCE FROM
                                                                                 NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
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                                                                                                                                                                                                                                                                                       SRAISGGP
                                                                                                                                                                                                                                                                                                                                  VGD--DFWCTDPSGDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAA
                                                                                                                                                                                                                                                                                                                                                            GGRENLEAADFLRQVNSVVYSYFP-
                                                                                                                                                                                                                                                                                                                                                                                  GGRVDLAKA-YYKAMTKSINKHFKGNGVIASMEHCNDF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPITK--
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                                                                                                                                                                                                                                                                                                               MHDMLDYFSMDP
                                                                                                                                                                                                                                                                                                                                                                                                          KEWGTLIFNYGRNEVRNFLVANALFWFDKYHIDGMRVDAVASMLYLDYCREEGEWVANEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPGLQMTMEDLA -- VDKIVLHKVGL -- -- VPPEKAEE -- -- -- MYEGLHAH -- -- -- --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GQKGMKAFIDELKGEFKTVEHVYV-----WHALCGYWGGLRPQVPG--LPEARVIQPVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D63999; BAA10073.1;
                                                                                                                                 OR AH6.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF02922; isoamylase_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00128; alpha-amylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000461; Alpha_amylase.IPR004193; Isoamylase_N.
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554
770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LVDKLIPYVKELGYTHIELLPIAEHPFDGSWG---YQVTGYYAPTSRFGSP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                1 N.A.
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                                                                                                                                                                                                                                                                 568
                                                                                                                                                                                                                                                                                       535
                                                                                                                                 1. 32, Created)
1. 32, Last sequence update)
1. 40, Last annotation update
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                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        433
486
554
                                                                                              Nematoda; Chromadorea; cinae; Caenorhabditis.
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EMBL; Z48007; CAA88054.1; -.
EMBL; Z48009; CAA88054.1; JO
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PS50011; PROTEIN_KINASE_DOM; 1.
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SEQUENCE OF
STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIPA_DROME P13217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                        SEQUENCE FROM N.A.
MEDLINE-88311074; PubMed-2457447;
Bloomquist B.T., Shortridge R.D.,
Montell C., Steller H., Rubin G.,
                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                              01-JAN-1990 (Rel. 13, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
101-NOV-1995 (Rel. 32, Last sequence update)
105-CCT-2001 (Rel. 40, Last annotation update)
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase
(EC 3.1.4.11) (Phosphoinositide-specific phospholipase C).
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SMART; SM00239; (
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PROSITE; PS50007; PIPIC_X_DOMAIN; 1.
PROSITE; PS50008; PIPIC_Y_DOMAIN; 1.
Hydrolase; Lipid degradation; Vision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed entities requires a license agreement (See )
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14:723-733(1988).

FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES DIACYLGLYCEROL (DAG) AND INOSITOL 1.4,5-TRISPHOSPHATE (IP3) IS MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPZ CENZYMES. NORPA IS INVOLVED IN PHOTOTRANSDUCTION.

CATALYTIC ACTIVITY: 1-phosphatidy1-1D-myo-inositol 4,5-bisphosphate + H(2)0 = D-myo-inositol 1,4,5-trisphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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SIMILARITY: DON
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  VGLVP.
                                            -PDRPLDPGLPLPPPCKLKRKILIKNKRMKPE--
                                                                                    GGLRPQVPGL---PEARVIQPVLSPGLQMTMEDLAVDKIVLH---
                                                                                                                                   DCAFVSSEYPVILSFENHCN-----RAQQYKLAKYCDDFFGDLLLKEPL
                                                                                                                                                             PCRLL--KFQENYKFRDYVNPKATGPRAGQKGMKAFIDELKGEFKTVEHVYVWHALCGYW
                                                                                                                                                                                                                       SSVEMYRQTLLAGC---RCVELDCWNGKGEDEEPIVTHGHAYCTEILFKDCIQAIA----
                                                                                                                                                                                                                                                                    GVIEGVRHLVDGGCPPGLVLIDDGWQSIGHDSDPITKEG---
                                                                                                                                                                                                                                                                                                                   MSLDGFKRYLMSDENAPVFLDRLD-----
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PF00387; PI-PLC-Y; 1.
PF00388; PI-PLC-X; 1.
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PLCYc; 1.
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                                            VEKVELELWLKGELKTDDDPEEDAS
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"Cytoplasmic 3-hydroxy-3-methylglutaryl coenzyme A synthase from the synthase from th
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01-0CT-1996 (Rel. 34, Last annotation update)
Hydroxymethylglutaryl-CoA synthase, cytoplasmic
synthase) (3-hydroxy-3-methylglutaryl coenzyme
HMGCS1 OR HMGCS.
Cricetulus griseus (Chinese hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires or send an email t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed
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Eukaryota; Metazoa; Chordata; Crania
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by non-profit institutions as long as
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                                                                                                                                                    1, L00334; AAA37076.1; 

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1, L00327; AAA37076.1; 

1, L00328; AAA37076.1; 

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                                PF01154;
IPR000590; HMG_COA_Synt.
1154; HMG_COA_Synt; 1.
PS01226; HMG_COA_SYNTHASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                            equires a license agreement (S email to license@isb-sib.ch).
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01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
01-CCT-1996 (Rel. 34, Last annotation update)
Hydroxymethylglutaryl-CoA synthase, cytoplasmic (EC 4.1.3.5) (HMG-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A synthase).
HMGCS1 OR HMGCS.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                           Ayte J., Gil-Gomez G., Hegardt F.G.;

"Nucleotide sequence of a rat liver CDNA encoding the cytosolic 3-hydroxy-3-methylglutaryl coenzyme A synthase.";

Nucleic Acids Res. 18:3642-3642(1990).

"IF FUNCTION: THIS ENZYME CONDENSES ACETYL-COA WITH ACETOACETYL-COA TO FORM HMG-COA, WHICH IS THE SUBSTRATE FOR HMG-COA REDUCTASE.

"IO FORM HMG-COA, WHICH IS THE SUBSTRATE FOR HMG-COA REDUCTASE."

"IO FORM HMG-COA, WHICH IS THE SUBSTRATE FOR HMG-COA COA - 
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                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Sprague-Dawley; TISSUE-Liver; MEDLINE-90301491; PubMed-1972979;
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                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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     SWISS-PROT entry
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Pfam; PF01154; HMG_CoA_synt; 1.
PROSITE; PS01226; HMG_COA_SYNTHASE; 1.
Lyase; Cholesterol biosynthesis; Multigene family.
ACT_SITE 129 129 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                     /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
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/cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
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US-09-819-993-5

US-09-819-993-5

US-08-305-505-6

US-08-717-515-8

US-08-525-654A-1

US-08-525-654A-1

US-09-004-838-131

US-09-004-838-131

US-09-004-838-103

US-09-004-838-103

US-09-05-505-4

US-09-305-505-4

US-09-134-078-28

US-09-134-078-28
                                                                                                                                                                               US-09-004-838-101
US-09-004-838-47
US-08-040-751-3
US-08-291-368-2
US-08-962-190-2
PCT-US-5-10310-2
5164180-4
                                                                                                                                                                                                                                                                      US-08-846-234-5
US-08-846-234-1
US-08-770-544-2
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                                                                                                                     Sequence 101, App
Sequence 47, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 6, Appli
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Sequence
                   1, Appli
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103, Appl
103, Appli
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
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US-09-298-924-6	US-09-242-690A-15	US-09-004-838-108	US-09-423-468A-15	US-09-134-001C-2980	US-09-313-677-17	US-09-313-677-19	US-09-313-677-2	US-09-313-677-21	US-09-066-047-5	US-08-403-853-10	US-08-810-712-10	US-09-423-468A-13	US-08-687-580B-7	US-09-364-970-8	US-09-388-743-22	PCT-US96-09193-2	US-09-307-185-5
Sequence 6, Appl1	Sequence 15, Appl	Sequence 108, App	Sequence 15, Appl	Sequence 2980, Ap	Sequence 17, Appl	Sequence 19, Appl	Sequence 2, Appli	Sequence 21, Appl	Sequence 5, Appli	Sequence 10, Appl	Sequence 10, Appl	Sequence 13, Appl	Sequence 7, Appli	Sequence 8, Appli		Sequence 2, Appli	Sequence 5, Appl1

RESULT 1 US-08-846-234-5

Sequence 5, Application US/08846234 Patent No. 6166292

GENERAL INFORMATION:

APPLICANT:

OSUMI Chieko

CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR

APPLICANT: NOZAKI Jinshi
APPLICANT: KIDA Takao
TITLE OF INVENTION: RAFFINOSE SYNTHASE GENE,
TITLE OF INVENTION: PRODUCING RAFFINOSE, AND
NUMBER OF SEQUENCES: 22

METHOD FOR TRANSGENIC PLANT

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TYPE: amino a TOPOLOGY: lir MOLECULE TYPE: US-08-846-234-5
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                     Matches
                                                                                                                                                          Best
                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                       TELEPHONE: (703)-413-3000
TELEFAX: (703)-413-2220
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 784 amino acids
                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
                                                                                                                                   y Match 100.0%; Score 4225; Local Similarity 100.0%; Pred. No. 0; hes 784; Conservative 0; Mismatches
                    61
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                                                                          MAPSFKNGGSNVVSFDGLNDMSSPFAIDGSDFTVNGHSFLSDVPENIVASPSPYTSIDKS 60
                    PVSVGCFVGFDASEPDSRHVVSIGKLKDIRFMSIFRFKVWWTTHWVGRNGGDLESETQIV 120
                                                       MAPSFKNGGSNVVSFDGLNDMSSPFAIDGSDFTVNGHSFLSDVPENIVASPSPYTSIDKS
amino acid
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                                                                                                                                                                                                                                                       Sequence 1, Application US/08846234 Patent No. 6166292
                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                    TITLE OF INVENTION: RAFFINOSE SYNTHASE GENE, TITLE OF INVENTION: PRODUCING RAFFINOSE, AND NUMBER OF SEQUENCES: 22
                                                                                                                                                                                               APPLICANT: OSUMI Chieko
APPLICANT: NOZAKI Jinshi
APPLICANT: KIDA Takao
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
OPERATING SYSTEM: PC-DOS.
                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                  STREET: 1755 S.
CITY: ARLINGTON
STATE: VIRGINIA
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                                                         COUNTRY: UZIP: 22202
                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVSD 540
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                                                                      USA
                                                                                                                             OBLON,
                                                                                                            N, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
 compatible
PC-DOS/MS-DOS
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                    TELEFAX: (716) 263-160
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703)-413-2220 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 600
FILING DATE: 21-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: GOLdman, Michael L.
REGISTRATION NUMBER: 30,72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
ETILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ling, Kai-Shu
APPLICANT: Ling, Kai-Shu
TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS
TITLE OF INVENTION: THEIR USES
TITLE OF SECUENCES: 32
                                                                                                                                                       REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA: APPLICATION NUMBER: US
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (703)-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC 244
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                 TYPE: amino STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Rochester
STATE: New York
                  TOPOLOGY:
                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
STREET: C
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                                                                     LENGTH:
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                                                  amino acid
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Y: U.S.A.
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GY: linear
                                                                      1390 amino acids
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                                                                                                                         (716) 263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (703)-413-2220
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                    linear
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                                                                                                                                            (716) 263-1304
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internal
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100.0%; Pred. No. 3.6e-12;
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US-09-251-645-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
SEQ ID NO 6
               APPLICANT: Kramer, Vance C.
APPLICANT: Morgan, Michael K.
APPLICANT: Anderson, Arne R.
APPLICANT: Hart, Hope
APPLICANT: Hart, Hope
APPLICANT: Unn, Martha
APPLICANT: Chen, Jeng S.
APPLICANT: Chen, Jeng S.
APPLICANT: Chen, Jeng S.
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: AND NUCLEIC ACID SEQUENCES CODING THEREFOR
FILE REFERENCE: CGC1963/A
CURRENT APPLICATION NUMBER: US/09/251,645
CURRENT APPLICATION NUMBER: US/09/251,645
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          958 YLAIGI 963
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hes 137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAPIGL 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --EVKGRSTYSIWCEQDYVRKCEWLRADNPVMALKPGYTPMTFEVVKAGTSEDAVVEYLK 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PISIEGVKTFAL----YLYQAKKLILSKPSQDLDIALDPFEFELITVSPVTKLIQTSLH 696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R---SMLYLHAGDD-PFALVKEAMKIVRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLT 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----KAVDKGKA-VVHAKEVKNVPVKTLPRGALKISED---TVRKELCMFRTCS
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                                                              684 --VSPVTKLIQTSLHFAPIGLV---NMLNTSGAIQSVDYDDDLSS-VEIGVKGCGEMRVF 737
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                  TLLSASEGVSQTNYSYFPSGVLQRESFLRDNKPISSGEYLYTMSGLIQRHKDSFGHNHVY
                                                                                                                                                 SIEGVKTFALYLYQAKKLILS-KPS---QDLDIAL-------DPFEFELIT- 683
                                                                                                                                                                                                                                                                    MLKIWNLNKFTGV-IGAFNCQGGGWCRETRRNQCFSQYSKRVTSKTNPKDIEWHSGENPI 643
                                                                                                                                                                                                                                                                                                                                               HAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGET 584
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                                                                                                                                                                                                                       LISALNVN---GTQLGALVYDGLG--------RVISDT-------
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                                                                                                                  -VGGRKTEYLYGPQGDKPIQSITPSHNKQNMDYLYYLGSVMSKFTTGTDQQNFRYHSKTG
                                                                                                                                                                                                                                                                                                                     HAT-----QIGYDVFDRIVKKTLPDGTILESAYASF-----SHEE
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Matches
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Best Local Similarity
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-078810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/781,734 FILING DATE: 10-JAN-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Shen, Kathy
APPLICANT: Meyers, Blake
TITLE OF INVENTION: Proce
TITLE OF INVENTION: Confe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
406 KIDVIHLLEMLC---
                                                           165
                                                                                                                                        120
                                                                                                                                                                             291
                                                                                                                                                                                                                                                       237 RHLVDGGCPPGLVLIDDGWQSIGHDS---DPITKEGMNQTV---AGEQMPCRLLKFQENY 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     980 SYDAQGRLVKTEQDAQYATFEYDNVGRLITTTKDTTSLSQLVTKIEY 1027
                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/004,838 FILING DATE: 09-JAN-1998 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1..487 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                           GLPIAIKTIALSLKGRSKSAWDVALSRLENHKIG -- SEEVVREVF -----
                                                                                                GLPEARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGV 405
                                                                                                                                      ---SILNIKVLKDVEGQSLFRQFAKNAGDDDLDPAFN----
                                                                                                                                                                           KFRDYVNPKATGPRAGQKGMKAFI-----DELKGEFKTVEHVYVWHALCGYWGGLRPQVP 345
                                                                                                                                                                                                                RFEADGGKNKFLVILDDVWQFVDLEDIGLSPLPNKGVNFKVLLTSRDSHVCTLMGAEAN- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101, Application US/09004838
5. 6350933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       487 amino acids
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                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Michelmore, Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Procedures and Materials for Conferring Pest Resistance in Plants
ED------YGGRVDL---AKAYYKAMT----
                                                                                                                                                                                                                                                                                                                  2.5%; Score 107; DB 4; Length 487; 20.1%; Pred. No. 0.035;
                                                                                                                                                                                                                                                                                                                                                                                             /note= "RG2G deduced sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101:
                                                                                                                                                                                                                                                                                             63; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #1
                                                                                                                                                                                                                                                                                             Indels 124;
                                                                                                                                  -GIADSIASRCQ 164
                                                         -KISYDNL 214
                  -KSIN 439
                                                                                                                                                                                                                                                                                             Gaps
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US-09-004-838-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δõ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              TELEFAX: (415) 576-03 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

COURTERS TWO Embarcadero Center, Eighth Floor
                                                                                                                                                   FEATURE:
                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Procedures
TITLE OF INVENTION: Conferring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
                                                                                          LOCATION: 1..488
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/781,734 FILING DATE: 10-JAN-1997
                                                                                                                              NAME/KEY:
                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                     STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                     NAME: Einhorn, Greg
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IYSCKRISLTCKGMSQFPKDLKFPNLSILKLMH-----GDKSLS----FPENFYGKME 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---LKIWNLNKFTGVIGAFNCQG 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVQVISYDKLMYPLLPSSLECSTNVRVLHLHYCSLRMFDCSSIGNLLNMEVLSFANSNIE 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VH------CANDSLWMGNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKH- 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KHFKGN--GVIASMEHCNDF---MFLGTEAISLGRVGDDFWCTDPSGDPNGTFWLQGCHM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94111-3834
                                                                                                                                                                                                                                                                                                                                                                     Einhorn, Gregory P. RATION NUMBER: 38,440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          San Francisco
                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -NFDLLKKLVLPDG-----SILRSEYYALPTRDCLFEDPLHNGETM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        California
                                                                                                                                                                                                                                          488 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Meyers, Blake
                                                                                                                                                                                                                                                                                                (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shen, Kathy
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                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Michelmore,
                                                                                                                                                                                                                                                                                                                   (415)
                                                                                                                                                                 protein
                 2.5%;
                                                                                                                                                                                                                                                                                                                 576-0200
                                                                                          /note= "RLG2G protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/09/004,838
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                                                                                                                                                                                                                                                                                47:
                                                                                                                                                                                                                                                                                                                                                       023070-078810US
Score 107; DB 4; Length 488; Pred. No. 0.035; Mismatches 167; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Materials for Pest Resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in Plants
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Matches

, 68

Conservative

63;

Indels 124;

Gaps

21;

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US-08-040-751-3
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                                                                                                                                                                                                                                                                                              SOFTWARE: PATEHLA.:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
DATE: 1930329
                                                                                                                                                                       FILING DATE: 19930329
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SALIMANCHIK, DAVID R.
REFERENCE/DOCKET NUMBER: MA39
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Payne, Jewel M
APPLICANT: Sick, August J
TITLE OF INVENTION: No. 5407825el Bacillus thuringiensis isolates
TITLE OF INVENTION: active against Lepidopteran Pests and Genes Er
TITLE OF INVENTION: Lepidopteran-active Toxins
                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1174 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID R. SALIWANCHIK
STREET: 2421 N.W. 41st STREET, SUITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
                                      TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: GAINESVILLE
STATE: FL
                      STRANDEDNESS:
                                                                                                                                                  TELEFAX: 904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WLPSTIGNLKKLR-LLDLTNCKG 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVQVISYDKLMYPLLPSSLECSTNVRVLHLHYCSLRMFDCSSIGNLLNMEVLSFANSNIE 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----NFDLLKKLVLPDG-----SILRSEYYALPTRDCLFEDPLHNGETM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VH-----CANDSLWMGNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKH- 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLFGSDDIGCVKMHDVVRDFVLHIFSEVQHASIVNHG------NVSEWLEENHS 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KHFKGN--GVIASMEHCNDF---MFLGTEAISLGRVGDDFWCTDPSGDPNGTFWLQGCHM 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QDEVTKSIFLLCALFPEDFDIPTEELVRYGWGLKLFIEAKTIREARNRLNTCTERLRETN 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIDVIHLLEMLC----ED-----YGGRVDL---AKAYYKAMT------KSIN 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLPIAIKTIALSLKGRSKSAWDVALSRLENHKIG--SEEVVREVF-----KISYDNL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLPEARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGV 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---SILNIKVLKDVEGQSLFRQFAKNAGDDDLDPAFN-----GIADSIASRCQ 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---LKIWNLNKFTGVIGAFNCQG 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IYSCKRISLTCKGMSQFPKDLKFPNLSILKLMH-----GDKSLS----FPENFYGKME 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KFRDYVNPKATGPRAGQKGMKAFI-----DELKGEFKTVEHVYVWHALCGYWGGLRPQVP 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RFEADGGKNKFLVILDDVWQFVDLEDIGLSPLPNKGVNFKVLLTSRDSHVCTLMGAEAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RHLVDGGCPPGLVLIDDGWQSIGHDS---DPITKEGMNQTV---AGEQMPCRLLKFQENY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                    single
                                                                                                                                                                                                                                                                                                                              US/08/040,751
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                                                                                                                                                                                                                                                                                                                                                                            Version
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; INDIVIDUAL ISOLATE:
; IMMEDIATE SOURCE:
; LIBRARY: Lambdagem -
; CLONE: 81A2
US-08-040-751-3
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                                                                                                                                                                                                                                                                                                          US-08-291-368-2
                                                                                                                                                                                                                                                         Sequence 2, Application US/08291368
Patent No. 5686069
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Best Local Similarity
                                                                                                                                                                                                                                       GENERAL INFORMATION:
                    APPLICANT: Payne, Jewel M.
APPLICANT: Sick, August J.
APPLICANT: Sick, August J.
TITLE OF INVENTION: No. 5686069el Bacillus thuringiensis Isolates
TITLE OF INVENTION: Active Against Lepidopteran Pests
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sallwanchik & Sallwanchik
ADDRESSEE: Sallwanchik & Saliwanchik
ADDRESSEE: Sallwanchik Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 336 YWGGLR-----PQVPGLPE------ARVIQPVLSPGLQMTMEDLA-----VDK 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       486
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                                                                                                                                                                                                                                                                                                                                                                                                 825 V-GCTDLQ------EDLG 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             710 YVTLPGTFDECYPTYLYQ--KIDESKLKAYNRYQLRGYIEDSQDLEIYLIRYNAKHETVN
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COUNTRY:
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Pred. No. 0
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ZIP: 32606 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

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Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/59
FILING DATE: 15-OCT-90
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (904)372-5800 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: PHYPOTHETICAL: YENANTI-SENSE: NO ORIGINAL SOURCE:
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LENGTH: 1174 amino acids
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REFERENCE/DOCKET NUMBER: MA50.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904)375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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LIBRARY: La...
NE: 81A2
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                    642 PISIEGV--KTFALYLYQAKKLILSK--
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                                                                                                                                                                                                                                                      495 VHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLV 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            314 YWAGHRVTSHFTGSSQVISSPQYGITANAEPSRTIAPSTFPGLNLFYRTLSDPFFRRSDN 373
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: si
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                                                                                              WCRETRRNQCFS-QYSKRVTSKTN----
                                                                                                                                    IPVDATFEAEYDLERAQKAVNSLFTS---SNQIELKTDVTDYHIDQVSNLV---DCLSDE 649
                                                                                                                                                              LPDGSILRSEY---YALPTRDCLFEDPLHNGETMLKI----WNLNKFTGVIGAFNCQGGG
                                                                                                                                                                                                                                                                                              FTGGDIIRTNVNGNVLSMSLNFSNTSLQRYRVRVRYAASQTMVMRVNVGGSTTFDQGFPS
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                                                        FCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDRGWRGSTDITIQGGDDVFKEN
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                                                                                                                                                                                                                                                                                                                                -----PNGTFWLQGCHM 494
                    -----PSQDLDIALDPF--EFELIT 683
Length 1174;
                                                                                              -PKDIEWHSG----EN 641
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                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (904)372-580 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1174 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 15-OCT-90
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                              IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                 MOLECULL Y HYPOTHETICAL: Y
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: No. 5985267el Bacillus thuringien TITLE OF INVENTION: Active Against Lepidopteran Pests
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                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
336 YWGGLR------PQVPGLPE------ARVIQPVLSPGLQMTMEDLA-----VDK 372
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                         LIBRARY: Lan
CLONE: 81A2
                                                                                                                                                                                                STRAIN: aizawai INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 2421 N.W. CITY: Gainesville
                                                    Local Similarity es 111; Conserv
                                                                                                                                                                                                                              ORGANISM:
                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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VENTION: No. 5985267el Bacillus thuringlensis Isolates
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                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           (904)372-5800
                                                                                                                                                                                                                                  Bacillus thuringiensis
                                                                                                                                                             Lambdagem -
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                                                    Score 107; DB:
Pred. No. 0.17;
82; Mismatches
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RESULT 10
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                                                                                                             COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VG
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10310
CLASSIFICATION: DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/:
FILING DATE: 15-OCT-90
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FAX NUMBER: (619) 453-6991
TITLE OF INVENTION: Protein Toxins Active Against Lepidopteran Pests
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                       ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite CITY: Gainesville
                                                                                                 FILING DATE
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PHONE NUMBER:
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CITY: San Diego
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                                                                                                                 PCT/US95/10310
                                                                                                                                                                                                                                                                                                                                                                                                                       IP: 92121
(619) 453-8030
(619) 453-6991
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LIBRARY: Lambd
CLONE: 81A2
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REFERENCE/DOCKET NUMBER: MA50.C1
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INDIVIDUAL ISOLATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                       VHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLV 554
V-GCTDLQ-
                                VKGCGEMRVFASKKPRACRIDGEDVG 753
                                                                                                                                                                                                                                        WCRETRRNQCFS-QYSKRVTSKTN----
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                                                                                                 VSPVTKLIQTSLHFAPIGLVNMLNTSGAIQSVDYDDDLS-----
                                                                                                                                   YVTLPGTFDECYPTYLYQ--KIDESKLKAYNRYQLRGYIEDSQDLEIYLIRYNAKHETVN 767
                                                                                                                                                                                                       FCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDRGWRGSTDITTIQGGDDVFKEN 709
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                                                                  VPGTGSLWPLSVE-SPIGRCGEPNR--CVPHLEWNPDLDCSCRDGEKCAHHSHHFSLDID 824
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RESULT 11 5164180-4

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US-08-846-234-2; Sequence 2, A
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                                                                                                                                                                                  vequence 2, Application US/08846234
Patent No. 6166292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 111;
                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                             APPLICANT: OSUMI Chieko
APPLICANT: NOZAKI Jinshi
APPLICANT: KIDA Takao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 353,860
FILING DATE: 18-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/451,389
FILING DATE: 14-DEC-1989
                                      CORRESPONDENCE ADDRESS
                                                      TITLE OF INVENTION: RAFFINOSE SYNTHASE GENE, TITLE OF INVENTION: PRODUCING RAFFINOSE, AND NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Payne, Jo
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374 IMPTLGINVVQGVGFIQPNNGEVLYRRRGTVDSLDELPIDGENSLVGYSHRL-----
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                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PISIEGV--KTFALYLYQAKKLILSK--------PSQDLDIALDPF--EFELIT 683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPVDATFEAEYDLERAQKAVNSLFTS---SNQIELKTDVTDYHIDQVSNLV---DCLSDE 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FTGGDIIRTNVNGNVLSMSLNFSNTSLQRYRVRVRXAASQTMVMRVNVGGSTTFDQGFPS
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OBLON, SPIVAK,
55 S. JEFFERSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jewel; Sick, August J.
N: BACILLUS THURINGIENSIS ISOLATES ACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.5%; Score 107; DB 6; 19.6%; Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82;
MCCLELLAND, MAIER & NEUSTADT, DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 181;
                                                                                               METHOD
                                                                            TRANSGENIC
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                                                                              PLANT
                    P.C.
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                                                                                                                                                                                                                                                                                                              ; ORGANISM: Human US-09-819-993-2
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                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Applicat
Patent No. 6436692
GENERAL INFORMATION:
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Best Local S
                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                            Query Match
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CURRENT FILING DATE: 2001-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: GONG, Fangcheng et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS,
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                LENGTH: 478
TYPE: PRT
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REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: NORMAN F. OBLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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LENGTH: 19 amino acids
 525
                                   136
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                                                                                                                                                                                             378 VGLVPPE-------KAE-EMYEGLHAHLEKVGIDGVKID------VIHL 412
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ZIP: 222
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                                                                                                     77
                                                                                                                                                                        17 VGIVALEIYFPSQYVDQAELEKYDGVDAGKYTIGLGQAKMGFCTDREDINSLCMTVVQNL 76
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                                                                                                                                                                                                                                          Local Similarity 18.9 es 77; Conservative
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                                     VF-
HAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGET
                                                                  ISLGRVGDDFWCTDPSGDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAF 524
                                                                                                     MERNNLSYDCIGRLEVGTETIIDKSKSVKTNLMQLFEESGNTDIEGIDTTN-ACYGGTAA
                                                                                                                                       LEM -- LCEDYGGRVDLAKAYYKAMTKSINKHF -- -- -- KGNGVIASMEHCNDFMFLGTEA 464
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(703)-413-2220
OR SEQ ID NO: 2:
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100.0%; Pr
1,700 0;
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Pred. No.
                                                                                                                                                                                                                                                          Score 102; DB 4; Length 478; Pred. No. 0.11;
                                                                                                                                                                                                                                             Mismatches
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. 0.00018;
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                                                                                                                                                                                                                                           Indels 190;
                                   -SSWDGLRGTHM----
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   584
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                                     156
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Qy 629 TNPKDIEWHSGENPISIEGVKTFALYLYQAKKLILSKPSQDLDIALDPEFELITVSPVT	Oy 465 ISLGRVGDDFWCTDPSGDPNGTFWLQGCHMVHCANDSLWMGNFIHPDMDMFQSTHPCAAF 1	Query Match Best Local Similarity 19.0%; Pred. No. 0.21; Matches 82; Conservative 59; Mismatches 111; Indels 180; G Qy 378 VGLVPPE	RESULT 14 US-09-619-993-5 Sequence 5, Application US/09819993 Patent No. 6436692 GENERAL INFORMATION: TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN TITLE OF INVENTION: THEREOF FILE REFERENCE: CLO01195 CURRENT APPLICATION UNMBER: US/09/819,993 CURRENT FILING DATE: 2001-03-29 NUMBER OF SEQ ID NOS: 5 SOPTWARE: FRastSEQ for Windows Version 4.0 SEQ ID NO 5 LENGTH: 518 TYPE: PRT ORGANISM: Human US-09-819-993-5	Db 157
LSKPSQDLDIALDPEFELITVSPVT 688 :	DSLWMGNFIHPDWDMFQSTHPCAAF 524 : SSWDGRYALVVAGDIAVY 163 . SSSWDGRYALVVAGDIAVY 163 . KHNFDLLKKLVLPDGSILRSEYYAL 568	DB 4; Length 518; 21; 21; 21; 21; 311; Indels 180; Gaps 20; 311; Indels 180; Gaps 20; 311; Indels 180; Gaps 20; 32; 33; 34; 35; 36; 37; 38; 38; 39; 30; 30; 30; 30; 30; 30; 30; 30; 30; 30	N ENZYME PROTEINS, AND USES	SKTINFKDIEWHSGENDIS 644 :

	3QW	Db 243	
	TNPKDIEWHSGENPISIEGVKTFALYLYQAKKLILSKPSODLDIALDPFEFE	Оу 629	
	4PIVDGKLSIQ	Db 214	
	PTRDCLFEDPLHNGETMLKIWNLNKFTGVIGAFNCQGGGW	Qy 569	
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		Qу 525	
	6 VFALVVAGDIAVY 163	Db 136	
	ISLGRVGDDFWCTDPSGDPNGTFWLQGCHMVHCANDSLWMGN	Qy 465	
	MERNNLSYDCIGRLEVGTETIIDKSKSVKTNLMQLFEE	Db 77	
		Qy 413	
	7 VGIVALEIYFPSQYVDQAELEKYDGVDAGKYTIGLGQAKMGFCTDREDINSLCMTVVQNL 76	Db 17	
	VGLVPPEKAE-EMYEGLHAHLEKVGIDGVKIDVI	Оу 378	
20;	atch 2.4%; Score 100; DB 1; Length 520; cal Similarity 19.0%; Pred. No. 0.22; 82; Conservative 59; Mismatches 111; Indels 180; Gaps 2	Query M Best Lo Matches	
	PE	; MOL US-08-30	
	STRANDEDNESS: single . TOPOLOGY: linear	 B S	
	TYPE: amino acid		
	INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:	; INFOR	
	114) 277-5591	· · ·	
	RMATION:	TEL	
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	n C.	. ATT	
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	APPLICATION DATA	; PRIOR	
	FILING DATE: CLASSIFICATION: 435	 O =	
	APPLICATION NUMBER: US/08/305,505	; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	
	SOFTWARE: PatentIn Release #1.0, Version #1.25	· · ·	
	patible		
	AG Z	COM	
	COUNTRY: TESCHISTIN		
	ITY: Milwaukee	 a O	
	ADDRESSEE: Quarles & Brady STREET: 411 East Wisconsin Avenue	 S Þ	
	NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS:	COR	
	OF INVENTION: STABILITY	TITLE	
	CANT: Miziorko, Henry M. OF INVENTION: 3-HYDROXY-3-METHYLGLUTARYL	; APPLI	
	INFORMATION:	; Patent No ; GENERAL	
	5,05-	US-08-305-5 ; Sequence	
	5	RESULT 1	

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Published_Applications_AA: *

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep: *

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep: *

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep: *

4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep: *

4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep: *

6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep: *

7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep: *

9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep: *

9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep: *

10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep: *

11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep: *

12: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep: *

13: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep: *

14: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep: *

14: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep: *
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4225
1 MAPSFKNGGSNVVS1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   April 4, 2003, 11:12:42; Search time 21 Seconds (without alignments) 2282.412 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAPSFKNGGSNVVSFDGLND.....QVPWPIDSSSGGISVIEYLF 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	و	80	7	σ	U	4	w	2	1	NO.	Result	
91.5	91.5	91.5	92.5	93	94	95.5	95.5	95.5	95.5	95.5	96	96	96.5	98	100	101.5	102	106.5	score		
2.2	2.2	2.2	2.2	2.2	2.2	2.3	2.3	2.3	2.3	2.3	2.3	۵. ن	2.3	2.3	2.4	2.4	2.4	2.5	массл		œ
781	557	304	1356	26926	1021	712	712	712	712	344	772	520	862	1431	518	626	478	905	Length		
9	10	10	9	9	9	10	10	10	10	10	ø	φ	9	12	9	12	9	10	. B	;	
US-09-866-050A-668	US-09-815-242-10114	US-09-970-638-4	US-10-077-111-10	US-09-759-508B-2	US-10-101-464A-954	US-09-771-161A-264	US-09-771-161A-263	US-09-771-161A-262	US-09-773-753-5	US-09-771-161A-173	US-10-121-032-28	US-10-193-295-4	US-09-978-522-1	US-10-095-718-4	US-10-193-295-5	US-10-001-851-27	US-10-193-295-2	US-09-728-721-52	HD		
Sequence 668, App	Sequence 10114, A	Sequence 4, Appli	Sequence 10, Appl	Sequence 2, Appli	Sequence 954, App	-	Sequence 263, App	Sequence 262, App	Sequence 5, Appli	Sequence 173, App	Sequence 28, Appl		Sequence 1, Appli	Sequence 4, Appli	Sequence 5, Appli	Sequence 27, Appl	Sequence 2, Appli	Sequence 52, Appl	Description		

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
86.5	86.5	87	87	87	87	87.5	87.5	88.5	88.5	89	89	89.5	89.5	89.5	89.5	89.5	89.5	90	91	91	91	91	91	91	91.5
2.0	2.0	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	2.1	$^{2.1}$	2.1	2.1	2.2	2.2	2.2	2.2	2.2	2.2	2.2
561	559	11877	11877	625	325	1410	559	538	525	559	350	1786	1786	1725	1482	1212	559	595	3472	3472	3472	809	802	378	859
10	12	10	9	10	10	9	12	9	9	10	9	10	9	9	10	10	12	9	9	9	9	9	9	10	9
US-09-925-301-1006	US-10-001-851-20	US-09-861-289-6	US-09-860-846-6	US-09-925-302-449	us-09-765-272-80	US-10-014-717-3	US-10-001-851-22	US-10-043-487-329	US-09-738-626-6109	US-09-908-855-15	US-09-738-626-4030	US-09-938-275-7	US-10-037-182-10	US-10-037-182-12	US-09-815-242-12484	US-09-815-242-5279	US-10-001-851-21	US-09-738-626-5826	US-10-027-801-4	US-10-034-623-4	US-10-027-806-4	US-10-080-114A-12	US-10-080-114A-2	US-09-816-664-7	US-09-978-522-3
Sequence 1006, Ap	Sequence 20, Appl	Sequence 6, Appli	Sequence 6, Appli	Sequence 449, App	Sequence 80, Appl	Sequence 3, Appli	Sequence 22, Appl	Sequence 329, App	Sequence 6109, Ap	Sequence 15, Appl	Sequence 4030, Ap	Sequence 7, Appl1	Sequence 10, Appl	Sequence 12, Appl	Sequence 12484, A	Sequence 5279, Ap	Sequence 21, Appl	Sequence 5826, Ap	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 12, Appl	Sequence 2, Appli	Sequence 7, Appli	Sequence 3, Appli

ALIGNMENTS

2004504	Qy 256QSIGHDSDPITKEGMNQTVAGEQMPCRLLKFQENYKFRDYVNPKA 300	Qy 215 FGWCTWDAFYLTVHPQGVIEGVRHLVDGGCPPGLVLIDDGW 255	QY 161 GSSKVVDASFRSMLYLHAGDDPFALVKEAMKIVRTHLGTFRLLEEKTPPGI-VDK 214	Query Match 2.5%; Score 106.5; DB 10; Length 905; Best Local Similarity 20.2%; Pred. No. 0.65; Matches 134; Conservative 90; Mismatches 203; Indels 235; Gaps	; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 52 ; LENGTH: 905 ; TYPE: PRT ; ORGANISM: Rattus rattus US-09-728-721-52	PRIOR FILING DATE: 1998-12-08 PRIOR APPLICATION NUMBER: US 09/099,041 PRIOR FILING DATE: 1998-06-17 PRIOR APPLICATION NUMBER: US 09/019,942 PRIOR FILING DATE: 1998-02-06 NUMBER OF SEO ID NOS: 71	222	9728721 LECULES OF THE CARD-RELATED
	KFRDYVNPKA 300 :: : : 242	LVLIDDGW 255: : : ISLLSDGQRY 194	KTPPGI-VDK 214 : : KECPGLGAPE 140	th 905; s 235; Gaps				PROTEIN FAMILY AND USES TH

9 352 VIQPVLSPGLOMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEK 290 VIQPTIGCEDITERFTGGLLAWGLVPPEKAEEMYEGLHAHLEK 290 VIQPTIGCEDITERFTGGLLAW
DLAWNFLMKVQALDSTARDSTLTPPEKAEEMYEGLHA
ROTE

	Qy 492 CH 493 	
¥	Qy 454CNDFMFLGTEAISLGRVGDDFWCTDPSGDPNGTFWLQG 491	
	QY 398 EKVGIDGVKIDVIHLLEMLCEDYGGRVDLAKAYYKAMTKSINKHFKGNGVIASMEH 453 : ::: : : : : : : Db 414 WRTGVNVLKRNSIRLAEVWLDDYKTYYYERINNQLGDFGDISSRKKLRED 463	
	Qy 368LAVDKIVLHKVG	
	Qy 325EHVYVMHALCGYWGGLRPQVPGLPEARVIQPVLSPGLQMTMED 367 :: :: :: : : : :	
	Qy 279 MPCRLLKFQENYKFRDYVNPKATGPRAGQKGMKAFIDELKGEFKTV 324	
	Qy 220 WDAFYLTVHPQGVIEGV-RHLVDGGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQ 278	
20;	Query Match 2.4%; Score 101.5; DB 12; Length 626; Best Local Similarity 21.3%; Pred. No. 1.1; Matches 77; Conservative 52; Mismatches 118; Indels 115; Gaps	
	NUMBEI SOFTWI SEQ ID LENG' TYPE ORGAI S-10-00	
	CURRE CURRE PRION PRION	
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	QY 705 MLNTSGAIQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRACRIDGEDVGFKYDQDQ 760	
	Cy 645 IEGVKTFALYLYQAKKLILSKPSQDLDIALDPEFELITVSPVTKLIQTSLHFAPIGLVN /04 Db 203QKEGNDKDFTLNDFGF-MIFHSPYCKLVQKSLARMLLND 240	
	585 MLKIWNLNKFTGVIGAFNCQGGGWCRETRRNQCFSQYSKRYTSKTNPKDIEWHSGENPIS 6 :: :: : : :: : : : :: :	
	Db 157	
	525 HAASRAISGGPIYVSDSVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGET	
	Db 136 VFNAVNWIESSSWDGLRGTHM 156	

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; LENGTH: 518
; TYPE: PRT
; ORGANISM: Human
US-10-193-295-5
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TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001195DIV
CURRENT APPLICATION NUMBER: US/10/193,295
CURRENT FILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: 08/819,993
PRIOR APPLICATION NUMBER: 08/819,993
PRIOR APPLICATION NUMBER: 08/819,993
PRIOR FILING DATE: 2001-03-29
INUMBER: OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
                                                                                                                                                                                  WS-10.7 5
US-10.95-718-4
Sequence 4, Application: US/10095718
; Patent No. US20020131956A1
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US-10-193-295-5
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APPLICANT: Walsh, Christopher APPLICANT: Chao, Hengjun APPLICANT: Burstein, Haim APPLICANT: Lynch, Carmel APPLICANT: Stepan, Tony APPLICANT: Munson, Keith TITLE OF INVENTION: Methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/10193295
Patent No. US20020173018A1
GENERAL INFORMATION:
APPLICANT: GONG, Fangcheng et al.
                                                                                                                                                               GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                              307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAASRAISGGPIYVSDSVG--------KHNFDLLKKLVLPDGSILRSEYYAL 568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEM--LCEDYGGRVDLAKAYYKAMTKSINKHF-----KGNGVIASMEHCNDFMFLGTEA 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGIVALEIYFPSQYVDQAELEKYDGVDAGKYTIGLGQAKMGFCTDREDINSLCMTVVQNL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----QW-----
                                                                                                                                                                                                                                                                                                                                                GEDVGFKYDQDQ 760
                                                                                                                                                                                                                                                                                                                                                                                             KLVQKSL--ARMLLNDFLN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISLGRVGDDFWCTDPSGDPNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAF 524
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Adeno-Associated Virus Vectors Encoding Methods of Using the Same
                                                                                                                                                                                                                                                                                                            317
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19.0%; Pred. No. 1.1;
/ative 59; Mismatches 111; Indels 180;
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                       Factor VIII
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RESULT 6
US-09-978-522-1
US-09-978-522-1
; Sequence 1, Application US/09978522
; Publication No. US20030033627A1
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CURRENT APPLICATION NUMBER: US/10/095,718
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 09/689,430
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/158,780
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 5
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Best Local S
Matches 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1431
TYPE: PRT
ORGANISM: canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          499
                                                                                                                                                                562 RSEYYALPTRDCLFEDPLHNGETMLKIWNLNKFTGVIGAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ---- PVSVGCFVGFDASEPDSRHVVSIGKLKDIRFMSIFRFKVWWTTHWVGRNGGDL--- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 NVVSFDGLNDMSSPFAIDGSDFTVNGH-----SFLSDVPENIVASPSPYTSIDKS----- 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 133; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVPGLPEARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGI 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSVFDENRSW--YLT-----ENMQRF-----
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                                                                                                                                                                                                                                                                                                                                                             GETVFMSMENPGLWVLGCHNSDFRNRGMTALLKVSSCNRNIDDYYEDTYEDIPTPLLNEN
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                                                                                                                                                                                                      -----DYGMSRSPH-----ILRNRAQSG-------DVQQFKKVVFQEFTDGS--
                                                                                                                                                                                                                                            GNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVSDSVGKHNFDLLKKLV---LPDGSIL 561
                                                                                                                                                                                                                                                                                     NVIKPRSFSQNSRHPSTKEKQLKMKREDFDIYGDYENQGLRSFQKKTRHYFIAAVERLW-
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                                                                                                                                                                                                                                                                                                                         -----CTDPSG-----DPNGTFWLQGC-----HMVHCANDSLWM 504
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19.0%; Pred. No. 8.
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                                                                                                                                                                                                                             RESULT 7
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                                                         GENERAL INFORMATION:
APPLICANT: GONG, Fangcheng et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS,
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 862
TYPE: PRT
ORGANISM: Vitis LOX 1
                                                                                                                                                                Sequence 4, Application US/10193295 Patent No. US20020173018A1
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APPLICANT: Irelan, Nancy
TITLE OF INVENTION: Lipoxygenase Genes From
FILE REFERENCE: 29520/37890
CURRENT APPLICATION NUMBER: US/09/978,522
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/241,220
FILE REFERENCE: CL001195DIV
CURRENT APPLICATION NUMBER: US/10/193,295
CURRENT FILING DATE: 2002-07-12
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                                                                                                                                                                                                                                                                                                                                 STHPCAAFHAASRAISGGPIYVSDSVGKHNF 547
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                                                                                 PROTEINS,
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RESULT 8
US-10-121-032-28
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PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                 Patent No. US20020155550A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 28, Application US/10121032
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TYPE: PRT
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                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEO for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:

ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: GLYCOSIDASE ENZYMES NUMBER OF SEQUENCES: 72
              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bylina, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLIQTSLHFAPIGLVNMLNTSGAIQSVDYDDDLSSVEIGVKGCGEMRVFASKKPRACRID 748
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                                  CLASSIFICATION: <Unknown>
                                               APPLICATION NUMBER: US/10/121,032 FILING DATE: 09-Apr-2002
                                                                                                                                                                                         COUNTRY: USA
ZIP: 92121
                                                                                                                                                                                                                             STATE: CA
                                                                                                                                                                                                                                          CITY: San Diego
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18.8%;
NUMBER:
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US/09/134,078
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Pred. No.
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Matches
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INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 772 amino acids
                                                                                                                                                                                                                                                                      510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 FRVWSPVSKWVKVLLFKNGEDTE-PYQVVNMEYKGNGVWEAVVEGDLDGVFYLYQLENYG 223
                                                                                                                                                                             554 GSINY------DGKLIKS--FALDPEETINYAACHDNHTLWDKNYLAAKADKKKEWT 602
                                                                                                                                                                                                                                                                                                                                                           451 YWVKEYHIDGFRFDQMGLIDKKTMLEVERALHKIDPTIILYGEPWGG-WGAPIRFGKSDV 509
                                                                                                                                                                                                                                                                                                                                                                                                   453 ------HCNDFMF--LG-TEAISLGRVGDDFWCTDPS----GDPNGTFW------L 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            412 --LLEMLCED-----YGGRVDLAKAYYKAMTKSINKHFKGNGVIASME------ 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 GLSHLVELG------VTH------332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 GVRHLVDGGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQMPCRLLKFQENYKFRD 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 GPKIEGYEDAIIYEIHIADITGLENS---GVKNK-----GLYLGLTEENTKGPGGVTT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 KIRTTVDP-----YSKAV-----YANNQESAVVNLARTNPEGWENDR 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 YVNPKATGPRAGQKGMKAFIDELKGEFKTVEHVYVWHALCGYWGGLRPQVPGLPEARVIQ 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 FKVW-----WTTHWVGRNGGDLESETQIVILEKSDSG------RPYVFLLPIVE--G 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 138; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/024002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 28:
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                                                                                                                                                                                                                                                                                                              QGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAASRA-ISGGPIYVSDS-----V 542
                                                                                                                                                                                                                                                                                                                                                                                                                                               YGIGELSAFDQTVPYYFYRIDKTGAY------LNESGCGN-VIASERPMMRKFIVDTVT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DPKNPHTRI - - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKAEEMYEGLHAHLEKVGIDGVKIDVIH--- 411
SYNAPISING 651
                                            SGENPISIEG 647
                                                                                      EEELKNAQKLAGAI-LLTSQGVPFLHGGQDFCRTTNFND---
                                                                                                                                                                                                                       GKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETM------LKIW- 589
                                                                                                                                                                                                                                                                      AGTH-VAAFNDE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----TG------DELDKDF---EKYYNW------GYDPYLFMVPEGRYST 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----EAMKIVRTHLGTERLLEEKTPPGIVDKFGWCTWDAFYL-----TVHPQGVIE
                                                                                                                                 ----NLNKFTGVIGAFNCQG-----GG--WCRETRRNQCFSQYSKRVTSKTNPKDIEWH 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 13-AUG-1998
APPLICATION NUMBER: 08/949,026
FILING DATE: 10-OCT-1997
APPLICATION NUMBER: 60/056,916
FILING DATE: 06-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.3%; Score 96; DB 9; Length 772; 20.6%; Pred. No. 4.8;
                                                                                                                                                                                                                                                                    -----FRDAIRGSVFNPSVKGFVMGG--YGKETKIKRGVV 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----REVKEMVKALHKH----GI-GVIMDMVFPHT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64; Mismatches 166;
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                                                                                      --N 641
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RESULT 10
US-09-773-753-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION UNMBER: U5/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR APPLICATION NUMBER: 13619
PRIOR APPLICATION NUMBER: 2000-04-12
PRIOR PILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
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US-09-771-161A-173
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APPLICANT: LEVINE, et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09773753
Patent No. US20020099177A1
GENERAL INFORMATION:
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Best Local :
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SEQ ID NO 173
LENGTH: 344
TYPE: PRT
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                                       ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/773,753

FILING DATE: 02-Feb-2001

CLASSIFICATION: CUNknown>

PRIOR APPLICATION: ADTA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 LYL-----HAGDDPFALVKEAMKIVRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVH 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 ETQIVILEKSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCV--ESGSSKVVDASFRSM 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 GFLPNGSLEDRLHCQTQACPP 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 ESSVSLLQ---GARPSPFCWPLCE-----ISRGTHNFSEELKIGEGGFGCVYRAVMRNT 234
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                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, N.W., SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: HUMAN IRAK-2
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: NI, JIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---PQGVIEGVRHLVDGGCPP 246
                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                               STATE: D.C
                                                                                                                                                                                                                                                                                                                                                     CITY: WASHINGTON
FILING DATE: <Unknown>
                   APPLICATION NUMBER: 08/980,060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUZIO, MARTA
DIXIT, VISHVA M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FENG, PING
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NUMBER OF SEQ ID NOS: 273
SOFTWARE: PatentIn version 3.0
SEQ ID NO 262
                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 262, Application US/09771161A Patent No. US20020110811A1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/771,161A CURRENT FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LEVINE, et al. TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES FILE REFERENCE: 802620-2005.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 135619
                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
    289
                                                                                                                    174 LYL-----HAGDDPFALVKEAMKIVRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVH 228
                                                                                                                                                                 184
                                        229 --- PQGVIEGVRHLVDGGCPP 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 ESSVSLLQ---GARPSPFCWPLCE-----ISRGTHNFSEELKIGEGGFGCVYRAVMRNT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 ETQIVILEKSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCV--ESGSSKVVDASFRSM 173
                                                                                                                                                                                                                                                                    Local Similarity
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mes 38; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: No. US20020099177A1 Relevant
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
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NAME: STEFFE, ERIC K.
                                                                                                                                                                                                     ETQIVILEKSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCV--ESGSSKVVDASFRSM 173
GFLPNGSLEDRLHCQTQACPP 309
                                                                              VYAVKRLKENADLEWTAVKQSFLTEVEQLSRFR-----HPNIVDFAGYCAQNGFYCLVY 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---PQGVIEGVRHLVDGGCPP 246
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                                                                                                                                                               ESSVSLLQ---GARPSPFCWPLCE-----ISRGTHNFSEELKIGEGGFGCVYRAVMRNT 234
                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
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; Pred. No. 4.7;
16; Mismatches
                                                                                                                                                                                                                                               16; Mismatches
                                                                                                                                                                                                                                                                Score 95.5; DB 10; Pred. No. 4.7;
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US-09-771-161A-264
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US-09-771-161A-263
                                                                                                                                                                              SEQ ID NO 264
LENGTH: 712
TYPE: PRT
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APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
                                                                             Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. US20020110811A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 264, Application US/09771161A
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Best Local Similarity
Matches 38; Conserv
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                                                             Matches
                                                                                                Query Match
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CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 13676
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
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PRIOR EILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
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CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
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                                                                                                                                                         ORGANISM: Homo sapiens
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                  116 ETQIVILEKSDSGRPYVFLLPIVEGPFRTSIQPGDDDFVDVCV--ESGSSKVVDASFRSM 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 VYAVKRLKENADLEWTAVKQSFLTEVEQLSRFR-----HPNIVDFAGYCAQNGFYCLVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 LYL-----HAGDDPFALVKEAMKIVRTHLGTFRLLEEKTPPGIVDKFGWCTWDAFYLTVH 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 ESSVSLLQ---GARPSPFCWPLCE-----ISRGTHNFSEELKIGEGGFGCVYRAVMRNT 234
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                                                                             Local Similarity
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Pred. No. 4.7;
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Pred. No. 4.7;
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RESULT 14
US-10-101-464A-954
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PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
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Best Local Similarity
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APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated f
TITLE OF INVENTION: and Their Use in the N
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 KVVDASFRSMLYLHAGDDPFALVKEAMKIVRTHLGTFRLLEEKTPPGIVDKFGWCTWDAF 223
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                                                                                                                              LQILIALSNYLLGPIPESL---GKCRSLERI--
                                                                                                                                                                   VDLAKAYYKAMTKSINKHFKGNGVIASMEHCNDFMFLGTEAISLGRVGDDFWCTDPSGD- 482
                                                                                                                                                                                                             QIVDLSSNKL----TGTLPPD------
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    ----SVGKHNFDLLKKLVLPDGSILRSEYYALPTRDCLFEDPLHNGETMLKI-WNLN
                                         PRGLFGLPELNQVE-FQDNLLVGEFPVSD-------DSIALKLGQITLSNNK 474
                                                                                   PNGTFWLQGCHMVHCANDSLWMGNFIHPDWDMFQSTHPCAAFHAASRAISGGPIYVSD--
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Best Local Similarity
Thehes 97; Conserve
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US-09-759-508B-2
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CURRENT APPLICATION NUMBER: US/09/759,508B
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/175,787
PRIOR FILING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 26926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09759508B publication No. US20020182599A1 GENERAL INFORMATION:
APPLICANT: Fishman, Mark C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13413 DGGSRIIGYVVDFLTEENKWQRVMKSLSLQYSAKDLTEGKEYTFR----VSAENENGEGT 13468
                                                                                                                                                                                                                                                                                                                                                                          13515 PSVSW-----KKGEDPLATDTRVSVESSAVNTTLIVYDCQKSDAGK-YTITLKNVAGT 13566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13469
                                         13710 ITGYHLEFKERNSLLWKRANKTPIRMRDF---KVTGLTEG-----LEYEFRVM--
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                                                                                                                          KYGYGEGLKSEPIVARHPFDVPDAPPPPNIV-----DVRHDSVSLTWTDPKKT-GGSP 13709
                                                                                                                                                                                                                                                  DPF-----ALVKEAMKIVRTHLG---TFRLLEEKTPPGIVDKFGWCTWDAFYLTVH 228
                                                                                                                                                                                                                                                                                            KEGTISIKVVGKPGIPTGPIKFDEVTAEAMTLKWAPPKDDGGSEITN------YILEKR 13619
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VYVWHALCGYWGGLRPQVPGLPEARVIQPVLSPGLQMTMEDLAVDKIVLHKVGLVPPEKA 386
                                                                                MPCRLLKFQEN-----YKFRDYVNPKATGPRAGQKGMKAFIDELKGEFKTVEH 326
                                                                                                                                                               PQGVIEGV-----RH---LVDGGCPPGLVLIDDGWQSIGHDSDPITKEGMNQTVAGEQ 278
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Gaps

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Title:
Perfect score:
Sequence:
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SUMMARIES

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ALIGNMENTS

TITLE JOURNAL	REFERENCE AUTHORS		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	E15707	RESULT 1
RAFFINOSE SYNTHASE GENE, PRODUCTION OF RAFFINOSE AND TRANSFORMED Patent: JP 1998084973-A 1 07-APR-1998; AJINOMOTO CO INC	<pre>1 (bases 1 to 2517) Oosumi,C., Nozaki,J. and Kida,T.</pre>	unclassified.	unidentified	unidentified.	JP 1998084973-A/1.	E15707.1 GI:5710390	E15707	Cucumis sativus mRNA for raffinose synthase, complete cds.	E15707 2517 bp DNA linear PAT 28-JUL-1999		

Pred. No.

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PN JP 1998084973-A/1
PD 07-APR-1998
PF 28-APR-1997 JP 1997111124
PR 26-APR-1996 JP 96P 107682, 26
PR 28-APR-1997 JP 107682, 26
PR 28-APR-1997 JP
GACGCGTTTTACCTAACGGTTCATCCACAGGGCGTAATAGAAGGCGTGAGGCATCTCGTC
                                       CGCTTGTTGGAGGAGAAGACTCCACCAGGTATCGTGGACAAATTCGGTTGGTGCACGTGG
                                                                                              CCGTTCCGAACCTCGATTCAGCCTGGGGATGATGACTTTGTCGATGTTTGTGTCGAGAGT
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         transformed plant
Patent; JP 199123080-A 1
AJINOMOTO CO INC
OS CUCUMIS SATIVUS (CUC)
PN JP 1999123080-A/1
PD 11-MAY-199
PF 24-OCT-1997 JP 19972
PR CHIEKO OZUMI, JINJI NV
PC C11N15/09, A01H5/00, C
Strandedness: Double;
CC Tppology: Linear,
FH Key
FT CDS
56.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Cuc
1 (bases 1 to 2569)
Chieko,O., Jinji,N. and Takao,K.
Raffinose synthase gene, process for producing raffir
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Raffinose
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JP 1999123080-A/1.
                                                                                        Cucumis sativus (Cucumber)
JP 1999123080-A/1
11-MAY-1999
                                       CHIEKO OZUMI,JINJI NOZAKI,TAKAO KIDA
C12N15/09,A01H5/00,C12N9/00//(C12N9/00,C12R1:19)
Andedness: Double;
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Location/Qualifiers
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Cucumis sativus
Cucumis sativus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
1 (bases 1 to 2569)
1 (bases 1 to 2569)
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Submitted (22-JUN-1998) Central Research Laboratories, Aajinomoto
Submitted (72-JUN-1998) Central Research Laboratories, Aajinomoto
Co. Inc., 1-1, Suzuki-cho, Kawasaki-ku, Kawasaki 210-8681, Japan
Location/Qualifiers
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Cucumis sativus raffinose
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527 c 643 g 755 t 3 others
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2036 CTTATCCTCTCCAAGCCCTCTCAAGATCTTGACATAGCTCTTGACCCATTCGAATTCGAATTCGAG 2095	Oy 901 ACCGGCCCCCGAGCCGGCCAGAAGGGGGATGAAGGGGTTTATAGATGAACTCAAAGGAAGA 960 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
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	Qy 541 GATCCGTTTGCACTTGTAAAGAGGCGATGAAGATCGTGAGGACCCATCTTGGAACTTTT 600
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	Oy 421 CCGTTCCGAACCTCGATTCAGCCTGGGGATGATGACTTTGTCGATGTTTGTGTCGAGAGT 480
1 SOLICATE COMMISSION OF THE SOLICATION OF THE S	OY 361 ATCCTTGAGAAGTCAGATTCTGGTCGACCGTATGTTTTCCTTCTTCCGATCGTTGAGGGA 420
441 GGTGLABACGGTAACGTTTTTGGTCTCAAGGATGTTAACATTTTGGTTGAACATTTAACAACGAACG	OY 301 TGGACTACACACTGGGTTGGTCGAAATGGTGGGGATCTTGAATCGGAGACTCAGATTGTG 360
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201 GANGGANGAGANT TOGCAAAGCATATTACAAAGCAATGAACAAATCAATTAAATAAA	OY 181 CCGGTTTCGGTTGCTTTGTTTGGATTCGACGCGTCGGAACCTGATAGCCGACACATGTT 240
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141 GTCCCGCCGGAGAAGGCTGAGGAGATGTACGAAGGACTTCATGCTCATTTGGAAAAAGTT 1 [QY 61 ATGTCGTCACCGTTTGCAATCGACGGATCGGATTCACTGTGAACGGTCATTCGTTTCTG 120 Db 116 ATGTCGTCACCGTTTGCAATCGACGGATCGGATTTCACTGTGAACGGTCATTCGTTTCTG 175 CW
L CTGCAGATGACGATGGAGATTTGGCGGTGGATAAGATTGTTCTTCATAAGGTCGGGCTG 1	OY 1 ATGGCTCCTAGTTTTAAAAAATGGTGGCTCCAACGTAGTTTCATTTGATGGCTTAAATGAC 60 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
021 CGCCCGCAGGTGCCTGGCTTGCCTGAGGCACGTGTGATTCAGCCAGTGCTTTCACCAGGG	Query Match 100.0%; Score 2352; DB 8; Length 2569; Best Local Similarity 100.0%; Pred. No. 0; Matches 2352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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S Eljiro, W. and Kenji, O.

Raffinose synthase gene

L Patent: JP 2000014389-A 1 18-JAN-2000;

SUMITOMO CHEM CO LTD

OS Brassica juncea

PN JP 2000014389-A/1

PD 18-JAN-2000

PF 10-DEC-1998 JP 1998351246

PR EIJIRO WATANABE, KENJI OEDA

PC C12N15/09, A01H5/00, C12N1/21, C12N5/10, C12N9/88, C1201/68// PC

(C12N9/88, C12R1:91), C12N15/00, C12R1:91), CC

(C12N9/88, C12R1:91), C12N15/00, C12N15/00, C12R1:91) CC

FH Key

FT CDS

Location/Qualifiers

1 260
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Raffinse synthase gene
E36417
E36417.1 GI:13019215
JP 2000014389-A/1.
Brassica juncea
Brassica juncea
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NAL Patent: JP 200016652-A 1 20-JUN-2000;

SUMITOMO CHEM CO LTD

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1362	3 GCTTTCCCCCGGTCTTGAGATGACAATGGAAGATCTAGCTGTGGATAAAATTGTTAATA	130
1127	8 GCTTTCACCAGGGCTGCAGATGACGATGGGGATGGAGATTTGGCGGTTGGATAAGATTGTTCTT	106
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1182	3 CCCAAATATTATGGGCCATGAGG	112
947	1 TCCCAAGGCCACCGGCCCCGAGCCGGCCAGAAGGGGGATGAAGGCGTTTATAGATG	89
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830 1062	4 CGGACACGATTCGGATCCCATCACCAAAGAAGGAATGAACCAAACCGTCGCCGGCGA	100
773 1002	4 TCTCGTCGACGGCGGTTGTCCTCCCGGTTTAGTCCTAAT	71 94
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416 642	3 CCTTGAGAAGTCAGATTCTGGTCGACCGTATGTTTTCCTTCCTTCCGATCGTTGA	5 8 5 8
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Mutant protein, its DNA and use thereof
Patent: JP 2001078783-A 1 27-MAR-2001;
SUMITOMO CHEMICAL CO LTD
OS Glycine max (soybean)
PN JP 2001078783-A/1
PD 27-MAR-2001
PF 03-JUL-2000 JP 2000200571
PF 03-JUL-2000 JP 2000200571
PR ELJIRO WATANABE, KENJI OEDA
PC C12N15/09, A01H5/00, C12N5/10, C12N9/10,
C12N5/00
CT
FH Key Location/Qualifiers
FT CDS (1): (2343).
                                         GACCCATCTTGGAACTTTTCGCTTGTTGGAGGAGAACACTCCACCAGGTATCGTGGACAA
                                                                              ATACGTCCACGTTGGCCATGACCCGTATCAGTTGCTTAGAGAAGCAACTAAAGTCGTTAG
                                                                                              GTATCTTCATGCTGGTGATGATCCGTTTGCACTTGTTAAAGAGGCGATGAAGATCGTGAG
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ATTCGGTTGGTGCACGTGGGACGCGTTTTACCTAACGGTTCATCCACAGGGCGTAATAGA
                          GATGCATTTGGGGACTTTCAAGCTTCTCGAGGAGAAAACCGCGCCAGTGATCGTAGACAA
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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Location/Qualifiers
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PN JP 1999215984-A/2
PD 10-AUG-1999
PF 12-DEC-1997 JP 1997342
PR EIJIRO WTANABE, KENJI C
PC C12N15/09, COTK14/415, C
C12O1/527,
PC C12O1/58, GO1N33/573//C
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University of Vienna, Althanstrasse 14, on Jan 16, 2002 this sequence version re
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                                                                   AGGCTTATAAAATATGAAGAGAATTATAAATTTAGAGAATACGAAAAT------
                                                                                                                                                       GATCCTGTTACAGAGCGAGATGGAATGAACCGAACCTCAGCTGGGGAACAAATGCCATGC
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sfrtslopglndyvdmsvesgsthvtgstfkaclylhlsndpyrlvkeavkviqtklg
sfrtslopglndyvdmsvesgsthvtgstfkaclychlsndpggckglygfvrd
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LVKIGVRGCGELSVFASEKPVCCKIDGVSVEFDYEDKMVRVQILWPGSSTLSLVEFLF
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Pred. No. 2.9e-274;
0; Mismatches 684;
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рь 1:	904 AAAAC IBTIGAACKAIGATTIKAIGITIIGACKAIGATTIGIGEGGAKKAITIGGGGGGGGTIGGG
Оу 10	24
Db 1:	225 CCTAAAGTGTGGAATGCCGGAAGCTAAGGTTGTTTCCGAAGCTGTCTCCGGGGGTG
Qy 1	.084 CAGATGACGATGGAGGATTTGGCGGGTGGATAAGGTTGTTCTTCATAAGGTCGGGC
Db 1:	.285 AAGATGACGATGGAGGATTTAGCGGTGGATAAGATTGTTGAGAATGGTGTGGGGCTAGTG
0у 1	144 CCGCCGGAGAAGGCTGAGGAGAGTGTACGAAGGACTTCATGCTCATTTGGAAAAAG
Db 1:	.345 CCTCCAAATTTGGCGCAGGAGATGTTTGATGGGATTCACTCTCATTTGGAGTCGGCGGGA
0у 1:	204 ATCGACGGTGTTAAGATTGACGTTATCCACCTATTGGAGATGTTGTGTAGAAGACTATGGA
Db 1	1405 ATTGACGGTGTTAAAGTTGACGTTATCCATTTGCTTGAGTTACTATCAGAGGAAT
Qy 1:	1264 GGGAGAGTGGATTTGGCAAAGGCATATTACAAAGCAATGACCAAATCAATAAATA
Db 1	1465 GGACGAGTTGAGCAAAAGCATATTACAAAGCACTAACCTCATCAGTGAACAAACA
Qy 1	1324 TTTAAAGGAAATGGAGTCATTGCAAGTATGGAACATTGTAACGACTTCATGTTCCT
Db 1:	1525 TTCAAAGGCAATGGTGAATTGCAAGCATGGAGCATTGCAATGACTTCTTTCT
0у 1	384 ACGGAAGCTATCTCTCTTGGTCGTGTTGGTGATGACTTTTGGTGCACGGACCCCTCTCGGT
Db 1	585 ACGGAAGCCATATCCCTCGGCCGCGTCGGAGATGATTTTTTGGTGCTGTGACCCCTC
Qy 1	1444 GATCCAAACGGTACGTTTTGGCTCCAAGGATGTCACATGGTTCATTGTGCCAACGACAGC
Db 1	1645 GATCCAAATGGTACATATTGGCTCCAAGGTTGTCACATGGTACATTGTGCCTACA
Фу 1	504 TIGTGGATGGGGAACTTCATCCACCCTGACTGGGATATGTTCCAATCCACCCAC
Db 1	1705 TTATGGATGGGAAATTTCATTCATCCAGATTGGGACATGTTTCAGTCCACCCAC
Qy 15	564 GCCGCCTTCCATGCTGCCTCTCGAGCCATCTCTGGTGGCCCGATCTATGTTAGTGATTCT
Db 17	65
0у 1	TGGGAAAGC
Db 1	825 GTTGGTAATCACAATTTCAAGTTGCTCAAATCTTTTGTTTTGCCCGACGGTTCTATCTTG
Оу 1	.684 CGAAGTGAGTACTATGCACTCCCGACTCGCGATTGTTTGT
Db 1	.885 CGTTGTCAACATTACGCACTCCCTACACGAGACTGCTTATTTGAAGACCCTTTGCATAAT
0у 1	.744 GGAGAAACTATGCTTAAGATTTGGAATTCTCAACAAGTTCACTGGAGTGATTGGTGCATTC
Db 1	945 GGCAAAACAATGCTCAAAATTTGGAATCTCAACAAATATGCTGGTGTTTTGGGTCTATTC
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Db 2	1005 AACTGCCAAGGTGGTGGTGGTGTCCTGAGACACGGCGAAACAAGAGCGCTTCTG
0у 1	.864 TCAAAACGAGTGACATCCAAAACTAAACCCAAAAGACATAGAATGGCACAGTGGAGAAAAC
Db 2	2065 TCACACGCGGTGACATGTTATGCAAGTCCTGAAGATATTGAATGGTGCAATGGAAAAACC
Ωу 1	.924 CCTATCTCTATTGAAGGCGTTAAAACCTTTGCGCTTTACCTCTATCAAGCCAAAAAACTT
Db 2	1125 CCAATGGACATCAAAGGTGTGGATGTTTTCGCTGTATTTTTTCAAGGAGAAGAACTG
0у 1	AGCTCTTGACCCATTCGA

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Best Local S
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AL Patent: JP 199215984 A 1 10-AUG-1999;
SUMITOMO CHEM CO LTD
OS VICIA fabb(broad bean)
PN JP 199215984 -A/1
PD 10-AUG-1999
PF 12-DEC-1997 JP 1997342899
PF 12-DEC-1997 JP 1997342899
PC C12N15/09,C07K14/415,C07K16/16,C12N1/21,C12N5/10,C12N
C1201/527,
PC C1201/68,G01N33/573//(C12N15/09,C12R1:91),(C12N1/21,C
PC C12N15/00,
PC C12N15/00,C12R1:91),(C12N15/09,C12R1:91),(C12N9/88,C12
PC C12N5/00,(C12N15/00,C12R1:91),(C12N15/00,C12R1:91)
PC C12N15/00,(C12N15/00,C12R1:91),(C12N15/00,C12R1:91)
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PC C12N15/00,C12R1:91),(C12N5/00,C12R1:91)
PC C12N15/00,C12R1:91)
PC C
                                                            AAGCTGAAGGATATTTCGGTTTATGAGTATTTTCAGGTTTAAGGTTTGGTGGACTACACAC
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Raffinose synthase gene a
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E24423.1 GI:13018163
JP 1999215984-A/1
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/db_xref="taxon:3906"
552 c 621 g
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1. .2746
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Pred. No. 2.9e-274;
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; Arabidopsis.
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Submitted (27-FEB-2002) DNA Sequencing and Technology Center,
Submitted University, 855 California Avenue, Palo Alto, CA 94304,
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Southwick, A., Karlin-Neumann, G., Nguyen, M., Lam, B., Miranda, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nguyen,M, (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SSP/Stanford) contributed equally to Location/Qualifiers
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Conservative

0;

Score 950.6; DB 8; Pred. No. 1.7e-272; 0; Mismatches 644;

Length Indels

45;

Gaps

4

40.48; 67.48;

29		1231	망
1275	AAGATTGACGTTATCCACCTATTGGAGATGTTGTGTGAAGACTATGGAGGGAG	N	Qy
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1215	CTGAGGAGATGTACGAAGGACTTCATGCTCATTTGGAAAAAGTTGGGATCGACGGTGTT	1156	Q
17		1111	Db
1155	AGGATTTGGCGGTGGATAAGATTGTTCTTCATAAGGTCGGGCTGGTCCCGGCGGAGAAG	1096	Qy
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930	ATCAA	88	Db
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582	ACCGGGTCGGAGTTTCGTCAGATTGTGTATGTCCATGCCGGGGATGACCCGTTCAAGCTC	523	Ър
555	GTTGATGCATCGTTCCGAAGTATGTTGTATCTTCATGCTGGTGATGATCCGTT	496	Qγ
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495	ATTCAGCCTGGGGATGATGACTTTGTCGATGTTTGTGTCGAG	436	Qy
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402	GAGAACGAGACTCAAATCATTCTTGATCAATCCGGGTCGGATTCTGGACCCGGATCC	34	ф
375	GAATCGGAGACTCAGATTGTGATCCTTGAGAA	340	Qy
4	ATATTCCGTTTCAAGGTTTGGTGGACTACTC	ω :	рь :
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282		2	Дb
279	GAACCTGATAGCCGACATGTTGTTTCGATTGGGAAGCTGAAGGATATTCGGTTTATC	220	Qy

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Submitted (14-NOV-2001) DNA Sequencing and Technology Center, Submitted (14-NOV-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Nguyen, M., Southwick, A., Karlin-Neumann, G., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chung, M.K., Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shinn, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 2718)
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OS Stachys sieboldii(Chinese artichoke)

PN JP 199215984-A/3

PD 10-AUG-1999

PF 12-DEC-1997 JP 1997342899

PF 212IRO WTANABE, KENJI OEDA

PC C12N15/09,C07K14/415,C07K16/16,C12N1/21,C12N5/10,C12N9/8

PC C12Q1/527,

PC C12Q1/58,G01N33/573//(C12N15/09,C12R1:91),(C12N1/21,C12R)

PC C12Q1/50,(C12R1:91),(C12N9/88,C12R1:91),(C12N9/88,C12R1:91)

PC C12N5/10,C12R1:91),(C12N9/88,C12R1:91),(C12N9/88,C12R1:91)

PC C12N5/00,(C12N15/00,C12R1:91),(C12N5/00,C12R1:91)

PC C12N5/00,(C12N15/00,C12R1:91),(C12N5/00,C12R1:91)
                                                TCGACCGTATGTTTTCCTTCCTTCCGATCGTTGAGGGACCGTTCCGAACCTCGATTCAGCC
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Eljiro,W. and Kenji,O.
Erfinose synthase gene and use thereof
Patent: JP 1999215984-A 3 10-AUG-1999;
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              TTGGAATCTCAACAAGTTCACTGGAGTGATTGGTGCATTCAACTGCCAAGGAGGAGGATG
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RESISTING, W. and Kenji, O.
Raffinose synthase gene
AL Patent: JP 2000014389-A 2 18-JAN-2000;

SUMITOMO CHEM CO LTD
OS Brassica napus
PN JP 2000014389-A/2
PD 18-JAN-2000
PF 10-DEC-1998 JP 1998351246
PR EIJIRO WATANABE, KENJI OEDA
PI (C12N15/09, A01H5/00,C12N1/21,C12N5/10,C12N9/88,C12R1:19), PC
(C12N1/21,C12R1:91),C12N15/00,C12R1:91),CC12N9/88,C12R1:19), PC
(C12N9/88,C12R1:91),C12N15/00,C12N5/00,C12R1:91) CC
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Chain Elongation of Raffinose in Pea Seeds: ISOLATION,
CHARCTERIZATION, AND MOLECULAR CLONING OF A MULTIFUNCTIONAL
CATALYZING THE SYNTHESIS OF STACHYOSE AND VERBASCOSE
J. Biol. Chem. 277 (1), 194-200 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTATGGATTGAAGGCTTTCACAAAGGATTTGAGGACAAAGTTCAAAGGTTTGGATGATG 1257
                                                                                                                                                                               TTTATGTTTGGCATGCTTTGTGTGGATATTGGGGTGGCCTTCGCCCGCAGGTGCCTTGGCT 1039
                        CCTCTCGAGCCATCTCTGGTGGCCCGATCTATGTTAGTGATTCTGTGGGAAAGCATAACT
                                                                                                                                                                                                                                                                               TGGGAAGAGTTGGGGATGATTTTTGGTTCCAAGATCCAAATGGTGATCCAATGGGAAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCCTGAGGCACGTGTGATTCAGCCAGTGCTTTCACCAGGGCTGCAGATGACGATGGAGG 1099
TGATTCAGCCTGATTGGGATATGTTCCAATCAGATCATGTTTGTGCTAAGTTTCATGCTG
                                                                                                                TTGGTCGTGTTGGTGATGACTTTTGGTGCACGGACCCCTCTGGTGATCCAAACGGTACGT 1459
                                                                                                                                                                                                                                                                                                                                                                       CAAAAGTTTACTATGAAGGATTGACAAAATCCATTGTCAAGAATTTTAATGGAAATGGAA
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SFSSICKPSESNAPPSLLQKVLAYSHKGGFFGFHETPSDFLMNSIGSFQKGKDFLSIF
RFKTWMSTQWIGKSGSDLQMETQWILIEVPETKSYVVIIPIIPIEKFRSALFPGFNDHV
KIIAESGSTKVKESTFNSIAYVHFSENPYDLMKEAYSALRVHLMSFRLLEEKTIPMLV
DKFGWCTWDAFYLTVNPIGIFHGLDDFSKGGVEPRFVIIDDGWOSISFDGYDPNEDAK
NUVLGGEQWSGKLHFFDECYKFRKYESGILLGPKSPYDPNNFTDLIKGIEHEKLRK
KREEAISKSSDLAE IESKIKVVKEIDDLFGGEOFFSGEKSEMKESYGLKAFTKOLR
TKFKGLDDYVWHALCGAWGGVRPETTHLDTKIVPCKLSPGLDGTWEDLAKVYEECLT
KSIVKNENGNGMIASWQHCNDFFFLGTKOISMGFWDDFWGDDFWGDPWGSFWLQGVH
MIHCSYNSLWMGQMIQPDWDMFGSDHVCAKFHAGSRAIGGGPIYVSDNVCSHDFDLIK
KLVFPDGTIPKCIYFPLPTROLFKNPLFDHTTVLKIMNENKYGGVIGAFNCQAGWD
PIMQKFRGFPECYKPLFTHDTKIVFTSHLWFNKYGGVIGAFNCQAGWD
PIMQKFRGFPECYKPLFDTHTVLKIMNENKYGGVIGAFNCQAGWD
PIMQKFRGFPECYKPLSYEVFWNQKGKGKFAPTGLTNNENGSGTVLDLEXVGNGAKIK
SEPIOFTIOPSTTELYSEVFWYNKLGGGIKKFAPTGLTNNENGSGTVLDLEXVGNGAKIK
VKGGGSFLAYSSESPKKFQLNGCEVDFEWLGDGKLCVNVPWHIEEACGVSDMEIFF"

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/db_xref="GI:13992585"
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57.7%;
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0; Mismatches 578;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGATITGATIAAGAAGCIIGIATICCCIIGATGGIACAATACCAAAATIGCATATATITC 1974
  TTCCTTGGATTGAAGAGGCTT
                                                                                                                                                                                                                                                                                                                                        CAGTGACCAAACTCCAAACTTCTCTACACTTTTGCCCCAATTGGGCTGGTGAACATGC 2116
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                         TGCCATGGCCAATTGATTCTT
                                                                                                                                                             TTAACACTAGTGGAGCCATCCAATCTGTGGACTATGACGATGACCTAAGCTCAGTCGAGA 2176
                                                                                                                                                                                                                                                                                                                 CCGTTACAAA---GTTATGTGGCGGCATCAAATTTGCACCAATTGGGTTGACAAACATGT
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                                                                               AGTTGAATGGTTGTGAAGTGGATTTTGAGTGGCTAGGTGATGGAAAATTGTGTGTCAATG
                                                                                                                     GTATTGATGGGGAGGATGTTGGGTTCAAGTATGATCAGGACCAAATGGTGGTGGTTCAAG
                                                                                                                                                                                                  TTGGTGTCAAAGGGTGTGGTGAGATGCGAGTATTTGCATCGAAAAAAACCAAGGGCTTGTC
                                                                                                                                                                                                                                        TCAACAGTGGTAGAACAGTTATAGATTTGGAATATGTTG-----GAAATGGTGCTAAGA
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Search completed: April Job time: 7057 secs ω 2003, 18:19:27

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Maximum Match 100%
Listing first 45 summaries
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Match Length
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Gapop 10.0 , Gapext 1.0
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2: /SIDS2/gcgdata/geneseq/geneseqn-embl/Na1981.DAT: *
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
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AAV40801
AAC89523
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AAV27438
AAC10002
AAV40800
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                                                                                                                                                                                                                                                                     Description
Soybean polynucleo
Nucleic acid encod
Broad bean raffino
                                                                                   Soybean raffinose
Sugarbeet raffinos
                                                                                                                                        Soybean raffinose
                                                                                                                                                                 Cucumber raffinose
Mustard raffinose
                                                                                                                                                                                                                   Cucumber raffinose
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cardiovascu	AAS35772	22	σ	1.6	37.4	45
Human cardiovascul	AAS35771	22	σ	1.6	7	44
Streptomyces averm	AAH79278	22	31422	1.6		43
S. avermitilis ave	AAA92302	21	31422	1.6	7.	42
11 for	AAD03343	22	911	1.6	w	41
Probe 10 for scree	AAD03342	22	911	1.6	ω	40
2	ABK69837	24	28046	1.6	8	39
Yeast AOD9604-asso	AAH24065	22	4590	1.6	38.8	38
Human ORF4040 cDNA	ABN79093	24	189	٠	8	37
Human thioredoxin	AAA53450	21	66566	•	9	36
Human cDNA sequenc	AAH18536	22	3408	1.7	9	35
Human stomach canc	AAI93894	22	3408	1.7	ø	3 4
DNA encoding novel	ABK11710	24	1417	1.7	9	33
Human cDNA differe	ABK84797	24	149671	•	œ.	32
\sim	AAS59516	23	29255	٠	۲.	31
plant	AAH87795	22	540		8	30
Peppermint plant o	AAH87794	22	636	٠	0	29
Corn tassel-derive	ABL73625	24	296		5	28
	AAX61259	20	253		90.8	27
Arabidopsis thalia	ABN98412	24	1036		Ü	26
Arabidopsis thalia	AAC42001	21	822		114	25
Nucleic acid encod	AAZ10004	20	993	7.2	169.6	24
raffinose	AAV40803	19	993		169.6	23
raffinose	AAD00331	21	1816	٠		22
raffinose sy	AAD00333	21	3060	•	œ	21
t raffinose s	AAD00337	21	2668			20
t raffinose	AAD00338	21	2653	•	•	19
raffinose	AAD00334	21	2842	10.2	•	18
	AAD00332	21	2868		•	17
	AAX61239	20	2780	٠	٠	16
	AAZ20207	20	928	12.9	٠	15
α.	AAZ20210	20	1762	•	•	14
Nucleic acid encod	AAZ10003	20	1762	•	•	13
æ	AAV40802	19	1762	37.7	886.8	12
raff	AAD00335	21	2524	40.3	•	11
Nucleic acid encod	AAZ10001	20	2746	40.7	•	10

RESULT 1 AAV22250 ID AAV2 Cucumber; raffinose synthase; sucrose; galactinol; ds Cucumber raffinose synthase cDNA. AAV22250 standard; cDNA to mRNA; 2517 06-JUL-1998 (first entry) AAV22250; ВP

ALIGNMENTS

WPI; 1998-264858/24. P-PSDB; AAW53570. Cucumis sativus 26-JUL-1996; 26-APR-1996; 07-APR-1998. JP10084973-A. 28-APR-1997; (AJIN) AJINOMOTO KK 96JP-0198079 96JP-0107682 97JP-0111124 Location/Qualifiers 56..2410 /product= raffinose_synthase /*tag=

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e present invention describes a raffinose synthase, having an activity forming raffinose from sucrose and galactinol. The raffinose synthase ne can be used for expression in a plant for the production of
                                                                                                raffinose synthase cose and galactinol
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30-APR-1998;
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10-DEC-1998;
This is the nucleotide sequence of a mustard cDNA clone coding for raffinose synthase (see AAY32074), a protein which can bind a D-galactosyl group through an alpha(1-6) bond to the hydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. The cDNA was
                                                                                   WPI; 199
P-PSDB;
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isolated from mustard (Brassica juncea) leaf cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see AAZ20207-10) may be used to obtain other raffinose synthase genes by labeled detection or amplification (claimed). These genes may be used to control the levels of raffinose produced in plants. Antisense genes can be used to knock out existing gene activity, and sense genes to increase the level of gene activity. The resulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, providing general health advantages. The sense and antisense genes may also be used in gene and phenotypic analysis of plants and for the selection of plant clones with the desired characteristics with respect to
raffinose
content.
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Sequence 2690 BP; 648 A; 608 C; 668 G; 765 T; 1 other;

44.38; 68.38;

DB 20; Length

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						ACGGACCCCTCTGGTGATC	GGAAATGGAGTCATTGCAAGTATGGAACATTGTAACGACTTCATGTTCCTTGGCACGG 	ATTTTA ATTTTG	> ->		 		1.04

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RESULT 4
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AC AAV4
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                    Claim 1;
                                                   New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
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                                                                                                                            P-PSDB;
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DB; AAW57887.
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                  31-34; 44pp;
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1642
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TGACTACGTCAATCCCAAGGCCACCGGCCCCCGAGCCGGCCAGAAGGGGGATGAAGGCGTT
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2498 BP; 650 A; 521 C; 673 G; 653 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                             ATTCGGTTGGTGCACGTGGGACGCGTTTTACCTAACGGTTCATCCACAGGGCGTAATAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGTCGCCGAGCAAATGCCCTGCCGTCTTTTGAAATTCCAAGAGAAATTACAAATTCCG
                                                                                                       GTGGCAAGCCATTTGTCACGACGACGAGGACCCATAACGGACCAAGAGGGTATGAAGCGAAC
                                                                                                                                                                                                                                                  AGGCGTGAGGCATCTCGTCGACGGCGGTTGTCCTCCCGGTTTAGTCCTAATCGACGATGG
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CTCCGCAGGGGAGCAAATGCCATGCAGGTTGGTGAAGTTGGAGGAAAATTACAAGTTCAG
                                                                                                                                                              TTGGCAATCCATCGGACACGATTCGGATCCCATCAC - - - CAAAGAAGGAATGAACCAAAC
                                                                                                                                                                                                                     AGGGGTGAAAGGGTTGGTGGAGGGAGGGTGCCCTCCAGGGATGGTCCTAATCGACGACGG
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Pred. No. 8.4e-304;
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01-SEP-1999;
                                                                     The present invention provides novel plant promoters which can be used the production of transgenic plants which express genes with desired
                                                                                                                      New soybean plant promoters useful for with desired properties -
                                                                                                                                                                                                                                                         27-APR-2000;
                                                                                                                                                                                                                                                                            02-NOV-2000
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                                                                                                                                                                                                                                                                                                                  Glycine
                                                                                                                                                                                                                                                                                                                                      Plant promoter;
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                                                                                                                                                                                                                                                                                                                                                                                                                      AAC89523 standard; DNA;
                                          Sequence
                                                                                                   Example 2; Page 24-28; 36pp; English
                                                                                                                                                      P-PSDB; AAB49400
                                                                                                                                                               WPI; 2001-104537/12
                                                                                                                                                                                   Ishige F,
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 41.5%;
nilarity 66.0%;
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                                          BP;
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99JP-0247211
                                                                                                                                                                                                                                                                                                                                     transgenic
                                          651 A; 521 C;
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 Score 976.4; DB 22;
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                                          673 G;
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                                          653 T; 0 other;
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1178	19 TGTTCTTCATAAGGTCGGGCTGGTCCCGCCGGAGAAGGCTGAGGAGGAGTGTACGAAGGACT	0у 11
1118 1182	TCAGCCAGTGCTTTCACCAGGGCTGCAGATGACGATGGAGGATTTTGGCGGTGGATAAGAT	Qy 1059 bb 1123
1058 1122	CAGGTGCCTGGCTTGCCTGAGGCACGTGTGAT 	ОУ 91 Db 101
998 1062	9 TATAGATGAACTCAAAGGAGAGTTTAAGACTGTGGAGCATGTTTATGTTTGGCATGCTTT	Qy 93 Db 100
938 1002	9 TGACTACGTCAATCCCAAGGCCACCGCCCCCGAGCCGCCAGAAGGGGATGAAGGCGTT	Qy 87
878 957	CETCGCCGGCGAGCAAATGCCCTGCTGTTTGAAATTCCAGAGAATTACAAATTCCG	
818 897	2 TTGGCAATCCATCGGACACGATTCGGATCCCATCACCAAAGAAGGAATGAACCAAAC	
761 837	02 AGGCGTGAGGCATCTCGTCGACGGCGGTTGTCCTCCCGGTTTAGTCCTAATCGACGATGG	Qy 7 Db 7
701 777	-42 ATTCGGTTGGTGCACGTGGGACGCGTTTTACCTAACGGTTCATCCACAGGGCGTAATAGA	7 6
641 717	82 GACCCATCTTGGAACTTTTCGCTTGTTGGAGGAGAAGACTCCACCAGGTATCGTGGACAA	Qy 5 Db 6
581 657	22 GTATCTTCATGCTGGTGATGATCCGTTTGCACTTGTTAAAGAGGCGATGAAGATCGTGAG	
521 597	62 CGATGTTTGTGTCGAGAGTGGTTCGTCGAAAGTTGTTGATGCATCGTTCCGAAGTATGTT	Qy 4 Db 5
461 537	02 TCTTCCGATCGTTGAGGGACCGTTCCGAACCTCGATTCAGCCTGGGGATGATGACTTTGT	Qy 4 Db 4
401 477	-45 GGAGACTCAGATTGTGATCCTTGAGAAGTCAGATTCTGGTCGACCGTATGTTTTCCT	Qy 3 Db 4
344 417	85 CAGGTTTAAGGTTTGGTGGACTACACACTGGGTTGGACTGGAATGGTGGGGATCTTGAATC	Qy 2 .pb 3
284 357	25 TGATAGCCGACATGTTGTTTCGATTGGGAAGCTGAAGGATATTCGGTTTTATGAGTATTTT	Qy 2 Db 2
224 297	65 TTCGATAGACAAGTCCCCGGTTTCGGTTGGTTTGTTTGGATTCGACGCGTCGGAACC	Qy 1 Db 2
164 237	17 TCTGTCCGATGTTCCTGAGAACATTGTTGCTTCTCTCTCT	Qy 1 Db 1
177		Db 1

2258 2322	99 GATGCGAGTATTTGCATCGAAAAAACCAAGGGCTTGTCGTATTGATGGGGAGGATGTTGG 	Оу 21 Db 22
2198 2262	39 ATCTGTGGACTATGACGATGACCTAAGCTCAGTCGAGATTGGTGTCAAAGGGTGTGGTGA	
2138 2202	TOTOTACACTITGCCCCAATTGGGCTGGTGAACATGCTTAACACTAGTGGAGCCATCCA	Qy 20 Db 21
2078 2142	19 TCTTGACCCATTCGAATTCGAGCTCATCACTGTTTCACCAGTGACCAAACTCATCCAAAC	
2018 2082	59 TTACCTCTATCAAGCCAAAAAACTTATCCTCTCCAAGCCCTCTCAAGATCTTGACATAGC	Qy 19 Db 20
1958 2022	99 CATAGAATGGCACAGTGGAGAAAACCCTATCTCTATTGAAGGCGTTAAAACCTTTGCGCT 	н н
1898 1962	39 CCGCAACCAATGCTTTTCACAATACTCAAAACGAGTGACATCCAAAACTAACCCAAAAGA	
1838 1902	79 GTTCACTGGAGTGATTGGTGCATTCAACTGCCAAGGAGGAGGATGGTGTCGTGAGACACG	
1778 1842	19 TTTGTTTGAAGACCCTTTGCATAATGGAGAAACTATGCTTAAGATTTGGAATCTCAACAA	Qy 17 Db 17
1718 1782	59 AGTGCTTCCTGATGGATCGATCCTTCGAAGTGAGTACTATGCACTCCCGACTCGCGATTG	Qy 16 Db 17
	99 TGGCCCGATCTATGTTAGTGATTCTGTGGGAAAGCATAACTTTGATCTTCTGAAAAAACT	<u> </u>
1598 1662	39 TATGTTCCAATCCACCCACCCTTGTGCCGCCTTCCATGCTGCCTCTCGAGCCATCTCTGG	
1538 1602	79 CATGGTTCATTGTGCCAACGACAGCTTGTGGATGGGGAACTTCATCCACCCTGACTGGGA	
1478 1542	419 CTTTTGGTGCACGGACCCCTCTGGTGATCCAAACGGTACGTTTTGGCTCCAAGGATGTCA	
1418 1482	59 TTGTAACGACTTCATGTTCCTTGGCACGGAAGCTATCTCTCTTGGTCGTGTTTG	
1358 1422	99 AATGACCAAATCAATAAATAAACATTTTAAAGGAAATGG. 	Qy 1 Db 1
1298 1362	39 GGAGATGTTGTGTGAAGACTATGGAGGGAGAGTGGATT' 	р д
1238 1302	179 TCATGCTCATTTGGAAAAGTTGGGATCGACGGTGTTAAGATTGACGTTATCCACCTATT	ப
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                                 This is the nucleotide sequence of a sugarbeet cDNA clone coding for raffinose synthase (see AN/32073), a protein which can bind a D-galactosyl group through an alpha(1-6) bond to the hydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. The cDNA was isolated from sugarbeet cv. haming leaf cDNA by PCR. Probes or PCR primers generated from plant raffinose synthase genes (see AN/22007-10) may be used to obtain other raffinose synthase genes by labeled detection or amplification (claimed). These genes may be used to control the levels of raffinose produced in plants. Antisense genes can be used to knock out existing gene activity, and sense genes to increase the level of gene activity. The cresulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, providing general health advantages. The sense and antisense genes may also be used in gene and phenotypic analysis of plants and for the selection of plant clones with the desired characteristics with respect to
                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-APR-1998;
30-APR-1998;
04-DEC-1998;
                                                                                                                                                                                                                                                                                                       New sense raffinose
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                                                                                                                                                                                                                                                                             Page 25-29; 55pp; English
                                                                                                                                                                                                                                                                                                      and antisense genes, useful in food plants -
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98JP-0351246.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                               GCTTTCACCAGGGCTGCAGATGACGATGGAGGATTTTGGCGGTGGATAAGATTTGTTCA
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                               GATGGTTTATTCATCAGAAAAGCCAAAAGCGTGTAGAGTTAATGGAGAAGACATGGAGTT
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P-PSDB; AAB98659.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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                                                                                                                                                                                                                                                  TAATTTGCCTTTGTCCATAACCCTAGAAGGATCAAATTTCCTCGCCAACGGCCACCCTTT 177
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                                                                  GGACGTTTGCATGGAGAGCGGGTCGACACGTGTCTGTGGGTCCAGCTTCGGGAGCTGCTT
                                                                                                                            TCTTCCGATCGTTGAGGGACCGTTCCGAACCTCGATTCAGCCTGGGGATGATGACTTTGT
                                                                                                                                                          CGAGACACAGATGATGCTTCTCGACAAAAACGACCAGCTCGGACGCCCCTTTGTGTTGAT
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 GACCCATCTTGGAACTTTTCGCTTGTTGGAGGAGAAGACTCCACCAGGTATCGTGGACAA
                                    GTATCTTCATGCTGGTGATGATCCGTTTGCACTTGTTAAAGAGGCGATGAAGATCGTGAG
                                                                                                               TCTCCCGATCCTCCAAGCCTCGTTCCGAGCCTCCCTGCAACCCGGTTTGGATTACGT
                                                                                                                                                                                  GGAGACTCAGATTGTGATCCTTGAGAAGTCAG---ATTCTGGTCGACCGTATGTTTTCCT
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                       ATACGTCCACGTTGGCCATGACCCGTATCAGTTGCTTAGAGAAGCAACTAAAGTCGTTAG
                                                                                         CGATGTTTGTGTCGAGAGTGGTTCGTCGAAAGTTGTTGATGCATCGTTCCGAAGTATGTT
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/product= "raffinose synthase"
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AGTGCTTCCTGATGGATCGATCCTTCGAAGTGAGTACTATGCACTCCCGACTCGCGATTG
                                       \tt TGGACCAGTTTACGTTAGTGATTGTGTTGGAAAGCACAACTTCAAGTTGCTCAAGAGCCT
                                                   TGGCCCGATCTATGTTAGTGATTCTGTGGGAAAGCATAACTTTGATCTTCTGAAAAAACT
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                                   24-JUN-1998
                                                                                                                                        Vicia faba
                                                                                                                                                             Raffinose synther gastrointestinal
                                                                                                                                                                                            Broad bean raffinose synthetase coding sequence
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                                                                                                                                                                                                                                                               AAV40800 standard; cDNA to mRNA;
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             18-DEC-1997;
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Best Local Similarity
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P-PSDB; AAW57886.
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This sequence encodes the broad bean raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides in the host organism or cell is changed. Raffinose ollgosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
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CCCATCACCAAAGAAGGAATGAACCAAACCGTCGCCGGCGAGCAAATGCCCTGCCGTCTT
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                                                TTCCATGCTGCCTCTCGAGCCATCTCTGGTGGCCCGATCTATGTTAGTGATTCTGTGGGA
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P-PSDB;
                                The present sequence encodes a raffinose synthase protein. sequence is isolated from plant material of broad beans. T protein forms raffinose by complexing alpha(1 to 6). D-gal hydroxyl group of the 6C of D-glucose residue in sucrose m
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18-DEC-1996;
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                    TGCTGCAAAATTGATGGGGTTAAGGTGAAATTTCTTTATG---AGGACAAAATGGCAAGA 2443
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                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                            The present sequence is a cDNA encoding raffinose synthase from clone sfll.pkl25.d4 isolated from a soybean immature flower cDNA library sfll. Raffinose synthase is involved in the biosynthesis of raffinose and higher homologues in the raffinose saccharide family from sucrose. The present sequence is useful for reducing the raffinose saccharide content of soybean seeds which improves the nutritional
                                                                                                                                                                                                                                                                                                                                                                                           Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids and encoded proteins involved in the biosynthesis of raffinose, useful for producing soybean seeds with a reduced raffinose content and therefore improved nutritional quality -
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence encodes the Japanese artichoke raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1762 BP; 395 A; 451 C; 499 G; 417 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 36-38; 44pp; English.
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DB; AAW57888.
                                                                                       ACCAGGTATCGTGGACAAATTCGGTTGGTGCACGTGGGACGCGTTTTACCTAACGGTTCA
                                                                                                                                          GGCGATGAAGATCGTGAGGACCCATCTTGGAACTTTTTCGCTTGTTGGAGGAGAAGACTCC
                                                                                                                                                                                                                                                                                 CAGGCCCTACATCGTGCTGCTTCCGCTCATCGAGGGGCAGTTTCGGGCCTTCCCCTTCAGCC
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                                                                                                                            CGCCGTGAAGGTGGCGCGCCACCACCTCGGGACGTTCAGGCTGCTGGAGGAGAAAACTCC
AGTCCTAATCGACGATGGTTGGCAATCCATCGGACACGATTCGGATCCCCATCACCAAAGA
                         GCCCCACGGCGTTATGGAGGGCGTGCAGGGGCTGGTTGACGGCGGATGTCCGCCGGGGCCT
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/product= raffinose synthetase
/note= "no stop codon given"
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                                                                                                                                                                              Matches 1223;
                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                        The present sequence encodes a raffinose synthase protein. The sequence is isolated from plant material. The protein forms raffinose by complexing alpha(1 to 6)- D-galactosyl hydroxyl group of the 6C of D-glucose residue in sucrose molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 13; Page 31-34; 40pp; Japanese.
                                                                                                                                                                                                                                                                               Sequence 1762
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18-DEC-1996;
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TCGACCGTATGTTTTCCTTCTTCCGATCGTTGAGGGACCGTTCCGAACCTCGATTCAGCC
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                                                                            AAACGGGTCGGATCTTGAGCGGGAAACTCAAATAGTCGTGCTCGACAAGTCCGA----CGA
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                                                                                                          TGCAAGTATGGAACATTGTAACGACTTCATGTTCCTTGGCACGGAAGCTATCTCTCTTGG
                                                                                                                                            ARTGTATGAAGGATTACATTCACATCTCGAATCTGTGGGGGATTGATGGAGTCAAAGTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the nucleotide sequence of a rapesed cDNA clone coding for raffinose synthase (see AAY32075), a protein which can bind D-galactosyl group through an alpha (1-6) bond to the hydroxy groatched to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. The cDNA was isolated from rapesed cv. Westar leaf cDNA by PCR. Probes or
               1087 ATGACGATGGAGGATTIGGCGGTGGATAAGATTGTTCTTCATAAGGTCGGGCTGGTCCCG
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                                                                                              GTTAACATGCTTAACACTAGCGGTGCGATTCGATCCTTGGTTTATCATGAGGA---
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RESULT 15
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                                                                                This is the nucleotide sequence of a soybean cDNA clone coding of raffinose synthase (see AAY3072), a protein which can bind a D-galactosyl group through an alpha(1-6) bond to the hydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. The CDNA was solven c. williams 82 immature seed cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see AAZ20307-10) may be used to obtain other raffinose synthase genes by labeled detection or amplification (claimed). These genes may be used to control the levels of raffinose produced in plants. Antisense genes to increase the level of gene activity. The and sense genes to increase the level of gene activity. The the growing conditions for gut enterobacteria, providing general chealth advantages. The sense and antisense genes may also be used in gene and phenotypic analysis of plants and for the selection of raffinose context.
 Query Match
Best Local Similarity
Matches 486; Conserv
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30-APR-1998;
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                                        Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK
Tel: 580 221 7391
Fax: 580 221 7380
                                                                                                          Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library Unpublished (2000)
                                                                                                                                                                                                               Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoldeae; Trifolieae;
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 Email: gdmay@noble.org
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BE248707 NF010D10D
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/dev_stage="Pooled timepoints"
/note-"Vector: Lambda Zap; Contains a mixture of entire
plantlets harvested in a series of days-post-watering
timepoints."

125 c 148 g 214 t
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/clone_lib="Drought"
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Location/Qualifiers
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NO. 1e-111;
                              Gossypium hirsutum cDNA 5' similar
[Cucumis sativus], mRNA sequence
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                                       TTTATGGATGGGCAACTTTATCCACCCTGATTGGGACATGTTCCAGTCCTCCCACCCTTG
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                                                                                      {	t TGCTGAGTTCCACGCTTCCAAGGGCCCATCTCCGGTGGCCCAATTTACATCANCGACAC}
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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Upton, NY 11973, USA
Tel: 516-344-3396
Fax: 516-344-3407
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primer: T3 Primer.
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/lab_host="XL1-Blue"
/note="Vector: pBluescript II
/ 139 c 149 g 193 t
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/tissue_type="immature fiber"
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/cultivar="Acala Maxxa"
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GAGATGGTGGGTGAGAAGTATGGTGGAAGAGTTGATTTGGCCAAAGCATATTACAAAGCT
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Contact: May GD
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BF636478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2510 Sam Noble Parkway, Ardmore,
Tel: 580 221 7391
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation
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ert Length: 649 Std Error: 0.00
be: 089 row: A column: 04
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Samuel Roberts Noble Foundation
One would parkway, Ardmore, OK 73402,
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/tissue_type="plantlets"
/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of
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/clone 11th="new"
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Plate: L48-11
Seq primer: T3
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Alzoaceae; Mesembryanthemum.
                                                                                                                                                                                                                                                                                                                                                     MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
                                                                                                                                                                                                                                                                                                                                                                                                      Department of Biochemistry University of Nevada
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BE131081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          common iceplant.
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            /dev_stage="Six week old"
/note="Vector: Lambda Uni-Zap
ECORI, Site_2: XhOI"
133 c 144 g 162 t
                                                                                                 /clone_lib="Ice plant Lambda Uni-Zap XR
, 48 hours NaCl treatment"
                                                                                                                                                 /organism="Mesembryanthemum crystallinum"
/db_xref="taxon:3544"
                                                                                 /tissue_type="Leaf, 48 h 0.4M
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Query Match

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458; Conser
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 Fax: 516-344-3407
Email: burr@bnlux
Seq primer: T3 Pri
                                                Tel: 516-344-3396
                                                           Brookhaven National Laboratory Upton, NY 11973, USA
                                                                                         Biology Department
                                                                                                         Unpublished (1999)
Contact: Ben Burr
                                                                                                                                                      Blewitt, M., Matz, E.C.,
                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids_II; Malvales; Malvaceae; Gossypium.
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               burr@bnlux1.bnl.gov
    T3 Primer
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Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzale Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tays from the Samuel Roberts N Medicago truncatula drought library
                                                                                    Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                   AACATGCTTAACACTAGTGGAGCCATCCAATCTGTGGACTATGACGATGACCTAAGCTCA
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The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
73402,
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Insert Length: 682 Std Error: 0.0
Plate: 061 row: C column: 04
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/db_xxe"="taxon:3880"
/clone="MPG1C04DT"
/clone_11b="Drought"
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/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Phaseoleae
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ID: Gm-c1068-3932 5'
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Public Soybean EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available through: ResGen, Invitrogen Corp. South Memorial Parkway Huntsville, AL 35801 For further in call: (800)-533-4363 or contact via email: ccu@resgen.com High quality sequence stop: 423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800 Fax: 314 286 1810
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/db_xref="taxon:3847"
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/clone_lib="Gm-c1068"
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                                                                                                                                                                      Contact: Wing RA
Clemson University Genomics
Clemson University
Clemson, SC
                                                                                                  Seq |
                                                                                                                                                             Tel:
                                                                                                                                                                                                                                                            Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T.,
,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, develop
                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                               Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                BF269676.1 GI:11200671 EST.
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                                                                                                il: rwing@clemson.edu
primer: TAATACGACTCACTATAGGG
n quality sequence stop: 563.
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864 656 4293
/db_xref="taxon:29729"
/clone="GA__Eb0005F08f"
                           /cultivar="8400"
                                          /organism="Gossypium
/strain="AKA"
                                                                                      Location/Qualifiers
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/tissue_type="Fibers isolated from bolls harvested 7-10 dpa"
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/note="Vector: pBK-CMV; Site_1:
a 143 c 124 g 145 t
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Glycine
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
Rosidae; eurosids I; Fabales; Fabaceae; Papil
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Tel:
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This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further i
call: (800)-533-4363 or contact: ccu@resgen.com web site:
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St.
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Contact: Shoemaker R/Public Soybean
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greenhouse grown"
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/clone_lib="Gm-c1068"
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/db_xref="taxon:3847"
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CAAAGTTGGGAGTCACAACTTTGAACTCCTCAAGACTTTGGTCTTGCCTGATGGGTGCAT
                                                                                               TTCTGTGGGAAAGCATAACTTTGATCTTCTGAAAAAACTAGTGCTTCCTGATGGATCGAT 1679
                                                                                                                                                                   TTGTGCCGCCTTCCATGCTGCCTCTCGAGCCATCTCTGGTGGCCCGATCTATGTTAGTGA 1619
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                                                                                                                                               TTGTGCTGCTTTTCATGCTGCCTCAAGAGCCATTTCTGGTGGACCAATCTATGTCAGTGA 183
                                                                                                                                                                                                                                         CAGTTTGTGGATGGGGAACTTCATCCACCCAGATTGGGACATGTTCCAGTCCACACACCC 123
                                                                                                                                                                                                                                                                                                                                        TGGTGACCCAAATGGCACATTTTGGCTGCAAGGGTGTCACATGGTGCACTGTGCCTACAA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The First Laboratory for Plant Gene Research Kazusa DNA Research Institute Yana 1532-3, Kisarazu, Chiba 292-0812, Japan Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S. Generation of 7137 non-redundant expressed seq legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AV421962 AV421962 AV421962 Lotus japonicus young plants (two-week old) japonicus cDNA clone MMM002b11_r 5′, mRNA sequence. AV421962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Lotus japonicus"
/db_xref="taxon:34305"
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75.5%;
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Pred. No. 4.6e-76;
0; Mismatches 119;
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Best Local
                                                                                     Matches
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1060 CAGCCAGTGCTTTCACCAGGGCTGCAGATGACGATGGAGGATTTGGCGGGTGGATAAGATT 1119
                                                      1000 TGTGGATATTGGGGTGGCCTTCGCCCGCAGGTGCCTTGGCTTGACGCACGTGTGATT 1059
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                            TGTGGTTATTGGGGTTGGGATAAGACCTAATGTTGAGGGTCTACCTGAAGCTATTGTGGAG
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                                                                                     375;
                                                                                                                                                                                                                                                                                                                                                                                                                    Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
OK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5', mRNA sequence.
BF636592
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: May GD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Torrez-Jerez, I., Scott, A.D., Harris, A.R., Gonzale Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D. Expressed Sequence Tays from the Samuel Roberts Nedicago truncatula drought library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
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                                                                                                                                                                                                                                                                                                                                  Seq
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                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                il: gdmay@noble.org
ert Length: 513 Std Error: 0.0
te: 090 row: H column: 02
primer: TCACACAGGAAACAGCTATGAC
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                                                                                    Conservative
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72 c
                                                                                                                                                                                                   /tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Con
                                                                                                                                                                                      plantlets harvested in a series of
                                                                                                                                                                                                                                                           /db_xref="taxon:3880"
/clone="NF090H02DT"
                                                                                                                                                                                                                                            /clone_lib="Drought"
                                                                                                                                                                                                                                                                                         /organism="Medicago truncatula"
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                                                                                                12.5%;
                                                                                    0,:
                                                                                  Score 293.4; DB 12;
Pred. No. 2.1e-75;
0; Mismatches 137;
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                                                                                                                                                                                                                 Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@em.agr.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mays
112
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                                                                                                                                                           /organism="Zea mays"
/cultivar="CO328"
                                                                                                                                             /db_xref="taxon:4577"
                                                                                                                                                                                                     Location/Qualifiers
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TGTAACGACTTCATGTTCCTTGGCACGGAAGCTATCTCTCTTTGGTCGTGTTGGTGATGAC 1419
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Singh, J.A., Wakui, K., Couroux, P., De Moors, A., Harris, L.J.,
J.I., Ouellet, T., Robert, L.S., Sprott, D. and Tinker, N.A.
Expressed Sequence Tags from Cold-Stressed Maize Seedlings
Unpublished (2001)
Contact: Singh, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG321136 818 bp mRNA linear EST 27-Zm04_O5d11_R Zm04_AAFC_ECORC_cold_stressed_maize_seedlings cDNA clone Zm04_05d11, mRNA sequence.

BG321136 BG321136 GI:13150814
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Agriculture and Agri-food Canada
KW Neatby Bidg., Central Experimental Farm,
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/tissue_type="Leaf, crown"
/note="Vector: Bluescript Sk-/XhoI-EcoRI; Site_1: Eco RI;
Site_2: XhoI; Lower temperature 50 C / hour from 22 to
120C; bring to 50 in 1 hour from 120C. Leave at 50C 2 day:
, photoperiod 16 hours. Light intensity was 125 uE-1.
Library prepared by in vivo mass excision from amplified
library."
300 c 230 g 129 t 47 others
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/clone_11b="Zm04_AAFC_ECORC_cold_stressed_maize_seedlings"
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                                                                                                         BM886707 528 bp mRNA linear EST 08-MAR-2002 sam29b05.yl Gm-c1068 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1068-6201 5' similar to TR:Q9ZT62 Q9ZT62 RAFFINOSE SYNTHASE ;,
                        EST
soybean
                                            BM886707.1
                                                                вм88670
                                                                                  mRNA sequence.
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Pred. No. 1.5e-69;
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                                              GAAGACCCTTTGCATAATGGAGAAACTATGCTTAAGATTTGGAATCTCAACAAGTTCACT 178:
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                        GCTGACCCTCTCCATGATGGCAAAACAATGCTCAAGATATGGAACCTCAACAAGTACACT
                                                                                                                                                                                           ATTTACATCAGTGACACAGTTGGGGAACCACAACTTTGAGCTGCTTAAGACCTTGGCCTTG 120
                                                                                                         CCAGATGGGTCCATCCTCAGATGTGAGCACTATGCACTCCCAACCAGGGACTGTCTCTTT
                                                                                                                               ATCTATGTTAGTGATTCTGTGGGAAAGCATAACTTTGATCTTCTGAAAAAACTAGTGCTT 1665
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1 (bases 1 to 528)

1 (bases 1 to 528)

Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna Shoemaker, R., Keim, P., Vodkin, L., Kucaba, T., Martin, J., Beck, C., A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 38801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
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Contact: Shoemaker R/Public
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/lab_host="DH10B"
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/clone_lib="Gm-cl068"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Shoemaker R/Public Soybean EST Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurl,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF425566 525 bp mRNA linear EST 06-DEC-2001 su44c11.yl Gm-c1068 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1068-2061 5' similar to TR:Q9ZT62 Q9ZT62 RAFFINOSE SYNTHASE;
                                                                                                                                                                                                                                                                                                                     This clone is available through: ResGen, Invitrogen Corp. South Memorial Parkway Huntsville, AL 35801 For further in call: (800)-533-4363 or contact via email: ccu@resgen.com Insert Length: 1160 Std Error: 0.00
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82. The month old greenhouse grown plants were deprived water for 3 days prior to harvesting the stressed leaf tissue. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI
                                                                           /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from mRNA isolated
from drought stressed leaf tissue of the cultivar Williams
                                                                                                                                                    /tissue_type="Leaf, drought stressed, 1 month old
greenhouse grown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:5840215
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Location/Qualifiers
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/clone_lib="A. thaliana, Ohio State clone set"
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/note="cDNA library was made from selected clones from the
Arabidopsis thaliana Ohio State clone set."
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US-09-383-630-5

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US-09-477-411A-45

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US-08-846-234-4
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-413-3000
TELEPAX: (703)-413-2220
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2517 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08846234 Patent No. 6166292
Query Match
Best Local Similarity
Matches 2352; Conserv
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APPLICANT: NOSMI Chieko
APPLICANT: NOSAKI Jinshi
APPLICANT: KIDA TAKAO
TITLE OF INVENTION: RAFFINOSE SYNTHASE GENE, METHOD FOR
TITLE OF INVENTION: PRODUCING RAFFINOSE, AND TRANSGENIC
                                                                                                                           MOLECULE TYPE: c
ORIGINAL SOURCE:
ORGANISM: cucu
FEATURE;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: NORMAN F. OBLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
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 Conservative
                                                                                                                                              cucumber (Cucumis sativas)
                                                                                                                                                                                                  linear
                                                                                                                                                                                 cDNA to mRNA
               100.0%;
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               Score 2352;
Pred. No. 0;
 Mismatches
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Indels
                                    2517;
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Gaps
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1140	.081 CTGCAGATGACGATGGAGGATTTGGCGGTGGATAAGATTGTTCTTCATAAGGTCGGGCTG 1	Qy
1135	GCCCGCAGGTGCCTGCCTGAGGCACGTGTGATTCAGCCAGTGCTTTCACCAGG	Db 1
080	.021 CGCCCGCAGGTGCCTGGCCTGAGGCACGTGTGATTCAGCCAGTGCTTTCACCAGGG 1	Qy 1
1020	961 TTTAAGACTGTGGAGCATGTTTATGTTTGGCATGCTTTGTGTGGGATATTGGGGTGGCCTT 1	Qy Db 1
01	01 ACCGGCCCCGAGCCGGCCAGAAGGGGATGAAGGCGTTTATAGATGAACTCAAAGGA 	Qу
900 955	841 TGCCGTCTTTTGAAATTCCAAGAGAATTACAAATTCCGTGACTACGTCAATCCCAAGGCC 9	Qy Db
340 395	781 GATTCGGATCCCATCACCAAAGAAGGAATGAACCAAACCGTCGCCGGCGAGCAAATGCCC 8	Оу
780 335		Qу
720 775	661 GACGCGTTTTACCTAACGGTTCATCCACAGGGCGTAATAGAAGGCGTGAGGCATCTCGTC 7	Оy
560 715	601 CGCTTGTTGGAGGAGAAGACTCCACCAGGTATCGTGGACAAATTCGGTTGGTGCACGTGG 6	Оy
500	541 GATCCGTTTGCACTTGTTAAAGAGGCGATGAAGATCGTGAGGACCCATCTTGGAACTTTT 6	ОУ
540	481 GGTTCGTCGAAAGTTGTTGATGCATCGTTCCGAAGTATGTTGTATCTTCATGCTGGTGAT 5	Оу
180 535	421 CCGTTCCGAACCTCGATTCAGCCTGGGGATGATGACTTTGTCGATGTTTTGTGTCGAGAGT 4	Оy
120 175	361 ATCCTTGAGAAGTCAGATTCTGGTCGACCGTATGTTTTCCTTCC	Qy
360 415	301 TGGACTACACACTGGGTTGGTCGAAATGGTGGGGATCTTGAATCGGAGACTCAGATTGTG 3	Qy ,
300 355	241 GTTTCGATTGGGAAGCTGAAGGATATTCGGTTTATGAGTATTTTCAGGTTTAAGGTTTGG 3	Qу
240 295	181 CCGGTTTCGGTTGGTTGGTTTGGATTCGACGCGTCGGAACCTGATAGCCGACATGTT 2	Qу
180 235	121 TCCGATGTTCCTGAGAACATTGTTGCTTCTCTCTTCTCCGTACACTTCGATAGACAAGTCC 1	ОУ
120 175	61 ATGTCGTCACCGTTTGCAATCGACGGATCGGATTTCACTGTGAACGGTCATTCGTTTCTG 1	Qу
50 115	1 ATGGCTCCTAGTTTTAAAAATGGTGGCTCCAACGTAGTTTCATTTGATGGCTTAAATGAC 6	Qу

Qy	Db	Qy	Qу	Oy Db	DB QY	Db	Qy	₽ 5	Вb	Qy	Db	Qy	Qу	Db	Qy	DЬ	Qy	Db	Qy	Db ·	Qy	Db	B	Qy	DЪ	Qy	Db	OV	Db
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CTAAGCTCAGTCGAGATTGGTGTCAAAGGGTGTGGTGAGATGCGAGTATTTGCATCGAAA 2		GGCTGGTGAACATGCTTAACACTAGTGGAGCCATCCAATCTGTGGACTATGACGATGA	CTCATCACTGTTTCACCAGTGACCAAACTCATCCAAACTTCTCTACACTTTGCCCCAATT 2 	CTTATCCTCTCCAAGCCCTCTCAAGATCTTGACATAGCTCTTGACCCATTCGAATTCGAG 2	AACCCTATCTCTATGAAGGGTTAAAACCTTTGGGTTTACCTGTATCAAGCCAAAAAA 1 	CTCAAAACGAGTGACATCCAAAACTAACCCAAAAGACATAGAATGGCACAGTGGAGAA	ACTCAAAACGAGTGACATCCAAAACTAACCCAAAAGACATAGAATGGCACAGTGGAGA	TICANCIBECANOSNOSAUSAISSISICSISAINANCHOSUSCANOSCOATISCIIIICANA TICIAILICANA TICIAILICANA TICIAILICANA TICIAILICANA TICIAILICANA TICAACTGCCAAGGAGGAGGATGGTGTGCTGTGAGACACGCCGCAACCAATGCTTTTCACAA 1	GGAGAAACTATGCTTAAGATTTGGAATCTCAACAAGTTCACTGGAGTGATTGGTGCA	ATGGAGAAACTATGCTTAAGATTTGGAATCTCAACAAGTTCACTGGAGTGATTGG	TCGAAGTGAGTACTATGCACTCCCGACTCGCGATTGTTTGT	TTCGAAGTGAGTACTATGCACTCCCGACTCGCGATTGTTTGT	TCTGTGGGAAAGCATAACTTTGATCTTCTGAAAAAACTAGTGCTTCCTGATGGATCGATC	GTGCCGCCTTCCATGCTGCCTCTCGAGCCATCTCTGGTGGCCCGATCTATGTTAGTGAT	GTGAT	AGCTTGTGGATGGGGAACTTCATCCACCCTGACTGGGATATGTTCCAATCCACCCAC	CTTGTGGGATGGGGAACTTCATCCACCCTGACTGGGATATGTTCCAATCCACCCAC	GGTGATCCAAACGGTACGTTTTGGCTCCAAGGATGTCACATGGTTCATTGTGCCAACGAC	GTGATCCAAACGGTACGTTTTGGCTCCAAGGATGTCACATGGTTCATTGTGCCAACGA		GCACGGAAGCTATCTCTCTTGGTCGTGTTGGTGATGACTTTTGGTGCACGGACCCCTC	CATTTTAAAGGAATGGAGTCATTGCAAGTATGGAACATTGTAACGACTTCATGTTCCTT 1	GAGGGAGTGGATTTGGCAAAGGCATATTACAAAGCAATGACCAAATCAATAAATA	GGATTTGGCAAAGGCATATTACAAAGCAATGACCAAATCAATAAATA	GGATCGACGGTGTTAAGATTGACGTTATCCACCTATTGGAGATGTTGTGTGAAGACTA	TCGACGGTGTTAAGATTGACGTTATCCACCTATTGGAGATGTTGTGTGAAGA		TCCCGCCGAGAAGGCTGAGGAGATGTACGAAGGACTTCATGCTCATTTGGAAAAAGTT	
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APPLICANT: ISHIGE, Fumiharu
APPLICANT: WATANABE, E1jiro
APPLICANT: OEDA, Kenji
TITLE OF INVENTION: PLANT PROMOTERS
FILE REFERENCE: 2185-0431P
CURRENT APPLICATION NUMBER: US/09/561,825
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: JP 11-124527
PRIOR APPLICATION NUMBER: JP 11-247211
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: JP 11-247211
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 23
I PRIOR FILING DATE: 1999-09-01
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Best Local Similarity 66.0%;
Matches 1507; Conservative
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LOCATION: (62)..(2407)
-09-561-825-23
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ORGANISM: Glycine
FEATURE:
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                                                           CGAGACACAGATGCTTCTCGACAAAAACGACCAGCTCGGACGCCCCTTTGTGTTJGAT
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US-08-232-463-14/c
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                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                        APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT
NUMBER OF SEQUENCES: 52
                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2380
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COUNTRY: USA
ZIP: 22313-0299
                                                STATE:
                                                                         CITY: Alexandria
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                                                                                                       Suite
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RESULT 4
US-09-457-046B-19
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Best Local Similarity
Watches 15; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; CLONE: pTZgpt-F1s
US-08-232-463-14
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic
FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEO ID NOS: 74
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                  Sequence 19, Application US/09457046B Patent No. 6287835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: TBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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APPLICATION NUMBER:
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linear
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APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 911
TYPE: DNA
ORGANISM: Taxus cuspidata
US-09-457-046B-21
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US-09-457-046B-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA ; ORGANISM: Taxus cuspidata US-09-457-046B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21, Application US/09457046B Patent No. 6287835 GENERAL INFORMATION:
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LENGTH: 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 1.6%;
Best Local Similarity 47.2%;
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                     557
                                                                                                                                                  581
                                                                                                                                                                                     437
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701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              317 TTGGTCGAAATGGTGGGGATCTTGAATCGGAGACTCAGATTGTGATCCTTGAGAAGTCAG 376
                                                                                                                                                                                                                                                                                                                                                                     1.6%;
Local Similarity 47.2%;
les 116; Conservation
                                                                                                                                                                                                                                                                                                                                   TTGGTCGAAATGGTGGGGATCTTGAATCGGAGACTCAGATTGTGATCCTTGAGAAGTCAG 376
ATAATG 706
                                   TTAAAG 562
                                                                                              TTGATGCATCGTTCCGAAGTATGTTGTATCCTTCATGCTGGTGATCATCCGTTTGCACTTG 556
                                                                                                                                                                                                                                                                                                    TTGTTATAAATGTTGACACCATAGAATATATGAAACAATGTGTTATGGAGGAATGTAATG 520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTAATCCCCCACTTCCAAATGGATATTATGGTAATGCCATTGGTACTGCATATGCAATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCAGCCTGGGGATGATGACTTTGTCGATGTTTGTGTCGAGAGTGGTTCGTCGAAAGTTG 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTCTGGTCGACCGTATGTTTTCCTTCCTTCCGATCGTTGAGGGACCGTTCCGAACCTCGA 436
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                                                                         TTAATCCCCCACTTCCAAATGGATATTATGGTAATGCCATTGGTACTGCATATGCAATGG
                                                                                                                                                TTCAAATTCCACATACTGAGAATGTGAAGCTTCTCTTTGCGATGGATTTGAGGAAATTAT 640
                                                                                                                                                                                 TTCAGCCTGGGGATGATGACTTTGTCGATGTTTGTGTGGAGAGTGGTTCGTCGAAAGTTG 496
                                                                                                                                                                                                                           ATTTTTGTTCGTCCTTTGAAGTAGTGGCAGCATTGGTTTGGATAGCAAGGACAAAGGCTC 580
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Pred. No. 0.065;
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                                                                                                                                                                                                                                                                                                                                                                             Indels
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APPLICANT: YE, Jane et al
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001058
CURRENT APPLICATION UMBER: US/09/740,035
CURRENT FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
US-09-010-928B-3
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                                                                                                                                                  CLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,928B
FILING DATE: 22-JAN-1998
CLASSIFICATION: 435
ATTORNEY/ACTAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Applic
Patent No. 5994099
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                                                                         ATTORNEY/AGENT INFORMATION:
NAME: MUTPIN JI., Gerald M
REGISTRATION NUMBER: 28977
REFERENCE/DOCKET NUMBER: 14
INFORMATION FOR SEQ ID NO: 3:
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                  COUNTRY: UNITED STATES OF ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART,
STREET: 8110 GATEHOUSE RD.
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APPLICANT: Hayashi, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
TITLE OF INVENTION: CODING THEREFOR
                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2824 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 8110 GATEHO
CITY: FALLS CHURCH
STATE: VIRGINIA
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Local Similarity 53.5%;
les 77; Conserva+1...
STRANDEDNESS:
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                  nucleic acid
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not relevant
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ISOLATED HUMAN PROTEASE PROTEINS,
NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS,
USES THEREOF
                                                                                                  1447-109P
                                                                                                                                                                                                                                                                                                                                                                                   AMERICA
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Pred. No. 1.3;
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SUITE 500E
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US-09-383-630-4/c
US-09-383-630-4/c
Sequence 4, Application US/09383630A
; Patent No. 6265632
; PAPPLICANT: Avner Yayon et al.
; APPLICANT: AVNER YAYON ET AL.
; TITLE OF INVENTION:
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                                     TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1085 AGATGACGATGGAGGATTTGGCGGTGGATAAGATTGTTCTTCATAAGGTCGGGCTGGTCC 1144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     918 CGTAGGACCTGGTGGTGCTGGTGGACCTTACGGACCTGGCGGTTCTGGACCTGGAGGTGC
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
COMPUTER READABLE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
                                                                                                   REGISTRATION NUMBER: 33,8
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-5625553
                                                                                                                                                                                                                                                                                                                                to an ASCI file CURRENT APPLICATION DATA:
                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 18 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGCGGAGCTGGAGCATGGTGGAGCATACGGACCTGGTGGATCATATGGACCTGGTGG 1037
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/383,630A FILING DATE: 26-Aug-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                    APPLICATION NUMBER: <Unknown>
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CITY: Arlington
                                                                               TELEFAX: 972-3-5625554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Mark M. Friedman c/o Anthony Castorina STREET: 2001 Jefferson Davis Highway, Suite 207
                                                                                                                                                                                     NAME:
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Word for Windows version 2.0 converted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States of America
LENGTH: 8083
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                                                                                                                                                                              Friedmam, Mark M
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taken from 3' region. Stop codon begins at position 2722."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHONDRODYSPLASIA
                                                                                                                                                                                                                                                                                                                                                                                                         Windows version 3.11
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Pred. No. 0.63;
                                                                                                                                                              33,883
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RESULT 9
US-09-383-630-5/c
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                                                                               US-09-383-630-5
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GENERAL INFORMATION:
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Best Local Similarity
Matches 87; Conserv
                                    Query Match
Best Local Similarity Matches 87; Conserv
                                                                                                                                                                                                                      TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Word for Windows version to an ASCI file CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,630A FILING DATE: 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: megabyte, 3.5" microdisk
                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 972-3-5625553
                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Avner Yayon et al.
TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH
FACTOR RECEPTOR ASSOCIATED
                                                                                                    SEQUENCE DESCRIPTION: SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAGGAATGAACCAAACCGTCGCCGGCGAGCAAATGCCCTGCCGTCTTTTGAAATTCCAA 861
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                                                                                                                      STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                             TELEFAX: 972-3-5625554
                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                         NAME: Friedmam, Mark M. REGISTRATION NUMBER: 33,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: MS DOS version 6.2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
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STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Mark M. Friedman c/o Anthony Castorina STREET: 2001 Jefferson Davis Highway, Suite 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                               LENGTH: 8083
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                  1.5%;
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Pred. No. 1.3
0; Mismatches
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Pred. No. 1.
                                    Score 36;
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                                                                                                    ID NO:
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                                        DB 4; Length 8083;
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Conservative

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; LOCATION: 183..2675
; OTHER INFORMATION: /product- "N. clavipes minor
; OTHER INFORMATION: ampullate silk protein"
US-08-209-747-1
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                                                                               Query Match
Best Local Similarity
Matches 77; Conserv
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COMPUTER: IBM PC COMPARTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/209,747
FILING DATE: 14-MAR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MUTCHY INFORMATION:
NAME: MUTCHY INFORMATION:
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-104P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2793 base pairs
                                     1029 GGTGCCTGGCCTGAGGCACGTGTGATTCAGCCAGTGCTTTCACCAGGGCTGCAGAT 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4857 AAGGGTTACTGTCTCCCACACTAAGCACCAGCAGGGGCTTGCCTCACCAAG 4806
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Colgin, Mark
TITLE OF INVENTION: cDNAs Encoding Minor Ampullate Spider
TITLE OF INVENTION: Silk Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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STREET: P.O. Box 747
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                           ORGANISM: Nephila clavipes TISSUE TYPE: minor ampullate gland
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GGTGCCGGAGCAGGAGCTGCTGCTGCTGCTGCTGCTGCAGGAGCAGGAGGTGCTGGT 1738
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                                                                                 Conservative
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                                                                                                 Score 35.6; DB Pred. No. 0.84;
                                                                                                                     DB 1; Length 2793;
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Best Local Similarity
Thes 77; Conserv
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US-08-458-298-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
                                    1679
1089 GACGATGGAGGATTTGGCGGTGGATAAGATTGTTCTTCATAAGGTCGGGCTGGTCCCGCC 1148
                                                                    1029 GGTGCCTGGCTTGCCTGAGGCACGTGTGATTCAGCCAGTGCTTTCACCAGGGCTGCAGAT 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 02-JUN-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: cDNAs encoding Minor Ampullate Spider TITLE OF INVENTION: Silk Proteins
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                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
ORGANISM: Nephila clavipes
                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lewis, Rando APPLICANT: Colgin, Mark
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                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 183..2675
OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                            TISSUE TYPE: minor ampullate gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Murphy Jr., Gerald M. REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER:
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CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                      GGTGCCGGAGCAGGAGCTGGTGCGGCTGCTGCTGGTGCAGGAGCAGGAGGTGCTGGT 1738
                                                                                                                                                                                                                                                                                                                                                                                                                   : 2793 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virginia
                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lewis, Randolph V
                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birch, Stewart, Kolasch & Birch
O. Box 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                         double
                                                                                                                              1.5%;
52.7%;
                                                                                                                                                                                                   /product= "N. clavipes minor
ampullate silk protein"
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                                                                                                                              Score 35.6; DB 1; Pred. No. 0.84;
                                                                                                            Mismatches
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                                                                                                            69;
                                                                                                                                             Length 2793;
                                                                                                            Indels
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; PAGES: 7120-7124
; DATE: Sept.-1990
; RELEVANT RESIDUES
US-08-425-069-1
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US-08-425-069-1
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 Best Local Similarity 49. Matches 94; Conservative
                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 28,977
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPAX: 703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Xu, Ming
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED |
TITLE OF INVENTION: PROTEIN,
TITLE OF INVENTION: CONTAININ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1149 GGAGAAGGCTGAGGAGATGTACGAAG 1174
                                                                                                                                                                                                                                PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: 301 No. 5728810th Washington Street CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                               OTHER INFORMATION:
                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 1...
                                                                                                                                                            TITLE: Structure of a protein superfiber: TITLE: drafline silk
                                                                                                                                                                                                                                                                                                                              ORGANISM: Nephilia clavipes
                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 19-APF
                                                                                                                                                 JOURNAL:
                                                                                                                                                                                              AUTHORS: Xu, Ming
AUTHORS: Lewis, Randolph V.
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAGGTGCAGGAGCAGGAGCTGGAGG 1824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08425069
                                                                                                                                Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         2338 base pairs
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'ON: 435
INFO-
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                                                                                IN SEQ
               1.5%;
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Score 35.2; D
Pred. No. 1;
0; Mismatches
   0;
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                                Length 2338;
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Gaps
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US-08-317-844B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           TELEX: 248345
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: MULPHY Jr., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 14
                                                PUBLICATION INFORMATION:
                                                          NAME/KEY: CDS
LOCATION: 1.2154
LOCATION: 1.2154
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                            HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                           MOLECULE TYPE: CD
                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703) 241-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                              FEATURE:
                AUTHORS:
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CITY: F
                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                           TYPE: nucleic acid STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                           TELEPHONE: (703) 241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 04-0CT CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSEE: Birch, Stewart, Kolasch & Birch T: 301 No. 5989894th Washington Street Falls Church : Virginia : Virginia RY: U.S.A.
Structure of a
                                                                                                                                                                                                                                                           2338 base pairs
              Lewis,
                               Xu, Ming
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                Randolph V.
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                                                                               /product= "Nephila clavipes
                                                             dragline
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protein superfiber:
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                                                             silk protein"
Spider
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VOLUME:

drafline silk .: Proc. Natl. Acad. Sci. U.S.A.

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CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 53
LENGTH: 1326
TYPE: DNA
ORGANISM: Taxus cuspidata
US-09-457-046B-53
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US-09-457-0468-53
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; DATE: Sept.-1990
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-317-844B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 53, Application US/09457046B
Patent No. 6287835
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REFERENCE: 53679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

Best Local Similarity 49.0

Matches 94; Conservative
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Best Local Similarity 46.3
Matches 114; Conservative
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                                                                                                                                                                                    437
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                                  557 TTAAAG 562
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                                                                                                                                                                                                                                                                                         686 TTGTTATAAAACGTTGACACCATAGAATATATGAAGCAATGTGTCATGGAGGAATGTAATG 745
                                                                                                                                                                                                                                                                                                                    317 TTGGTCGAAATGGTGGGGATCTTGAATCGGAGACTCAGATTGTGATCCTTGAGAAGTCAG 376
 926
                                                                                                                                                                                                                      746 AATTTTGTTCGTCTTTTGAAGTAGTGGCAGCATTGGTTTTGGATAGCACGGACAAAGGCTC 805
                                                                                           TTGATGCATCGTTCCGAAGTATGTTGTATCTTCATGCTGGTGATGATCCGTTTGCACTTG 556
                                                                                                                                                                                TTCAGCCTGGGGATGACTTTGTCGATGTTTGTGTCGAGAGTGGTTCGTCGAAAGTTG 496
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ATAATG 931
                                                                      TTAATCCCCCACTTCCAAATGGATATTATGGTAATGCCATTGGTACTGCATATGCAATGG
                                                                                                                                             TTCAAATTCCACATACTGAGAATGTGAAGCTTCTCTTTGCGATGGATTTGAGGAAATTAT 865
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Pred. No. 1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  Score 34.8; DB 4; Length 1326; Pred. No. 0.92; 0; Mismatches 132; Indels 0
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RESULT 15

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Search completed: April Job time: 249 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Johnson, William G.
APPLICANT: Stenroos, Edward S.
APPLICANT: Stenroos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING,
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
FILE REFERENCE: 601-1-057
                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 11
LENGTH: 18596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/09318448 Patent No. 6210950
                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/318,448
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                     5157 CCTGGGAGGTGGAGGGTGCCGTGAGCCACGATCGCGCCATTGCACTCCAGCCTGGGCAAC 5216
                                                                                                                                                                                                           1809 CCAAGGAGGAGGATGGTGTGTGAGACACGCCGCAACCAATGCTTTTCACAATACTCAAA 1868
                                                                                5217 AAGAGCGAAACTCTCAAAAAAACAAAAAAAAAGGATGGGTTCCATATGGGTG 5266
                                                                                                                        1869 ACGAGTGACATCCAAAACTAACCCAAAAGACATAGAATGGCACAGTGGAG 1918
                                                                                                                                                                                                                                               1.5%;
Local Similarity 57.3%;
les 63; Conservarion
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                                                                                                                                                                                                                                                                                                DB 4;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
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      Published_Applications_Na:*

1: /cgn2_6/ptodata/2/pubpna/U
2: /cgn2_6/ptodata/2/pubpna/U
3: /cgn2_6/ptodata/2/pubpna/U
4: /cgn2_6/ptodata/2/pubpna/U
6: /cgn2_6/ptodata/2/pubpna/U
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9: /cgn2_6/ptodata/2/pubpna/U
10: /cgn2_6/ptodata/2/pubpna/U
11: /cgn2_6/ptodata/2/pubpna/U
12: /cgn2_6/ptodata/2/pubpna/U
13: /cgn2_6/ptodata/2/pubpna/U
14: /cgn2_6/ptodata/2/pubpna/U
15: /cgn2_6/ptodata/2/pubpna/U
16: /cgn2_6/ptodata/2/pubpna/U
17: /cgn2_6/ptodata/2/pubpna/U
18: /cgn2_6/ptodata/2/pubpna/U
19: /cgn2_6/ptodata/2/pubpna/U
11: /cgn2_6/ptodata/2/pubpna/U
12: /cgn2_6/ptodata/2/pubpna/U
13: /cgn2_6/ptodata/2/pubpna/U
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2352
1 ATGGCTCCTAGTTTTAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        April 3, 2003, 18:19:36; Search time 248 Seconds (without alignments) 8318.946 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          593429 segs, 438583890 residues
//cgn2_6/ptodata/2/pubpna/VGCUS_FUBCOMB.seq:*
//cgn2_6/ptodata/2/pubpna/VGCUS_FUBCOMB.seq:*
//cgn2_6/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
//cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
//cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
//cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
//cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
//cgn2_6/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
//cgn2_6/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
//cgn2_6/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
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                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                               cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16 17 18 19	c 113 114	1 W 4 W 10 V & 0	Result
37 37 37 36.8	37.4 37.4 37.4 37.4	755 445. 45. 388 388	Score
1.000	1	111113	Query Match
5222 5696 5757 750	46050 1664 1664 1664 1664	296 377 160 911 911	Query Match Length DB
10 10 9	910991	10 9 01 10	10
US-09-993-170-57 US-09-993-170-60 US-09-993-170-56 US-10-184-644-104	US-09-80-09-80-1271 US-10-091-504-1271 US-10-091-504-1272 US-10-091-504-1272 US-09-764-869-1271 US-09-764-869-1272 US-09-796-692-7801	US-09-294-0938-2999 US-09-878-574-1840 US-09-878-574-1840 US-09-866-570A-19 US-09-866-570A-21 US-09-866-572A-19 US-09-866-572A-19	ID US-09-770-445-180
Sequence 57, Appl Sequence 60, Appl Sequence 56, Appl Sequence 104, App	Sequence 2.1, Appli Sequence 3. Appli Sequence 1271, Ap Sequence 1272, Ap Sequence 1271, Ap Sequence 1272, Ap	Sequence 299), Ap Sequence 1840, Ap Sequence 410, Appl Sequence 19, Appl Sequence 21, Appl Sequence 21, Appl	Description Sequence 180, App

Query Match 4.8%; Best Local Similarity 62.9%; Matches 175; Conservative

Score 113.2; DB 10; Length 1036; Pred. No. 6.2e-25; 0; Mismatches 103; Indels 0;

Gaps

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45	44	43	42	41	40	39	38	37	36	35 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
33.8	34	34	34	34.2	34.2	34.6	34.8	34.8	34.8	34.8	34.8	34.8	34.8	34.8	35	35	35	35	35	35.2	35.4	35.4	36	36.2	30.8
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US-09-815-242-7419	US-10-263-788-1	US-09-070-927A-129	US-09-815-242-6833	US-09-764-847-1426	US-10-092-154-1426	US-09-901-136-3	US-09-967-768A-119	US-09-880-107-1590	US-09-954-531-348	US-09-954-531-124	US-09-866-572A-53	US-09-866-570A-53	US-10-184-644-346	US-09-867-701-6593	US-09-816-093-3	US-10-274-873-3	US-09-764-847-1680	US-10-092-154-1680	US-10-025-380-1125	US-10-184-644-402	US-10-071-766-85	US-09-822-846-199	US-09-811-825-3	US-09-864-761-11473	US-10-014-502-3
Sequence 7419, Ap	Sequence 1, Appli	Sequence 129, App	Sequence 6833, Ap	Sequence 1426, Ap	Sequence 1426, Ap	Sequence 3, Appli	Sequence 119, App	Sequence 1590, Ap	Sequence 348, App	Sequence 124, App	Sequence 53, Appl	Sequence 53, Appl	Sequence 346, App	Sequence 6593, Ap	Sequence 3, Appl1	Sequence 3, Appli	Sequence 1680, Ap	Sequence 1680, Ap	Sequence 1125, Ap	Sequence 402, App	Sequence 85, Appl	Sequence 199, App	Sequence 3, Appli	Sequence 11473, A	Sequence 3, Appli

ALIGNMENTS

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; LENGTH: 1036
TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-445-180
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US-09-770-445-180/c
                                                                 SOFTWARE: FOR SEQ ID NO 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 180, Application US/09770445 Patent No. US20020023281A1
                                                                                                                  APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2023US (PARA 012PRV)
CURRENT APPLICATION NUMBER: US/09/770,445
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
                                                                                                                                                                                                                                                                                                APPLICANT:
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APPLICANT:
                                                                                                            PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                 Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
                                                                               FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
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                                                                                                                                                                                                                                                                 Davis, Keith R. Allen, Keith
                                                                                                                                                                                                                                                                                             Slader,
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Slader, Ted
                                                                                                                                                                                                                                                                                                                                 Garcia, Carlos A.
                                                                                                                                                                                                                                                                                                                                                                                                                 Page, Amy
                                                                                                                                                                                                                                                                                                                                                                                                                                    Yu, Yang
Rameaka, Joshua G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gorlach, Jorn
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US-09-294-093B-2999; Sequence 2999, Ap
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; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-020-Q1-B1-B11
US-09-878-574-2803
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APPLICANT: LA ROSA, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules an
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
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SEQ ID NO 2803
LENGTH: 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 151;
                                                                                                                                                                                                                               1656 ACTAGTGCTTCCTGATGGATCGATCCTTCGAAGTGAGTACTATGCACTCCCGACTCGCGA 1715
                                                                                                                                                                                                                                                                                                                                                                                                    1536 GGATATGTTCCAATCCACCCACCCTTGTGCCGCCTTCCATGCTGCCTCTCGAGCCATCTC 1595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1476 TCACATGGTTCATTGTGCCAACGACAGCTTGTGGATGGGGAACTTCATCCACCCTGACTG 1535
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                                                                                                                                                                                                                                                                                                                                                                                                                                             91 TCACATTGCATCAGTGGCTTACAATACTATTTTCCTTGGTGAATTTATGCAGCCAGACTG 150
                                                                                                                                               TTGTTTGTTTGAAGACCCT 1734
                                                                                                                                                                                          GCTTGCACTACCTGATGGTTCTATATTAAGGGCTAAACTTCCAGGACGACCAACAAAGGA
                                                                                                                                                                                                                                                                                                TGGTGGCCCGATCTATGTTAGTGATTCTGTGGGAAAGCATAACTTTGATCTTCTGAAAAA 1655
                                                                                                                                                                                                                                                                                                                                                             GGATATGTTTCATAACCTACATCCGATGGCTGAATATCATGGTGCAGCACGAGCTGTATG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGATGTCCAATTTATGTCAGTGACAAGCCCGGACACCATGACTTTGATCTTTTGAAGAA
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                                                                                                          TTGCTTATTTACTGATCCT
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Application US/09294093B
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APPLICANT: Tha Rosa, Thomas J.
APPLICANT: Thampson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules :
TITLE OF INVENTION: Plants
FILE REFERENCE: 38 -21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-878-574-1840
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: LOCATION: 190, 193-194, 206, 217, 232,
: OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-2999
                                                                                                                                                           US-09-878-574-1840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
SOFTWARE:
SEQ ID NO 2999
FRIGTH: 296
                                                                                                                                                                         SEQ ID NO 1840
LENGTH: 377
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: LIB3028-032-Q1-B1-E5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. US20010051335A1 GENERAL INFORMATION:
                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1840, Application Patent No. US20020110548A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: April 21,1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNICLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
FILE REFERENCE: PL-0009 US
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217
                                   192 TGGTTGCTTTGTTGGATTCGACGCGTCGGAACCTGATAGCCGACATGTTGTTTCGATTGG 251
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                                                                            Local Similarity
les 89; Conserv
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TGGGGCATTCATTGGGGTTCAATCCCATCACAAGGGTAGCCGCACAGTCTTCCCAATTGG 276
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                                                                            Conservative
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                                                                                             1.9%;
55.3%;
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                                                                          Score 45.8; DB 10;
Pred. No. 0.00068;
0; Mismatches 72;
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Pred. No. 2.4e-13;
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                                                                                                             Length 377;
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                                                                                                   RESULT 6
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; ORGANISM: Arabidopsis thaliana
US-09-770-696-410
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              Sequence 19, Application US/09866570A
Patent NO. US20020168745A1
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
AITTLE OF INVENTION: Transacylases of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version SEQ ID NO 410
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Best Local Similarity 57.0%;
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APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2031US (PARA-020PRV)
CURRENT APPLICATION NUMBER: US/09/770,696
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,278
PRIOR APPLICATION NUMBER: 60/178,278
PRIOR FILING DATE: 2000-01-27
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FILE REFERENCE:
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|131 TGTGTATTGGAGACTTTGGGTG 152
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Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
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Rameaka, Joshua G
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Slader, Ted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Allen, Keith
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                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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53679
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                Transacylases of the
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Pred. No. 0.001;
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                Paclitaxel Biosynthetic Pathway
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; TYPE: DNA
; ORGANISM: Taxus cuspidata
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; Sequence 21, Application US/09866570A

; Patent No. US20020168745A1
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SEQ ID NO 21
LENGTH: 911
TYPE: DNA
ORGANISM: Taxus cuspidata
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Best Local :
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SEQ ID NO 19
LENGTH: 911
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/866,570A
CURRENT FILING DATE: 2001-05-25
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CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US/09/457,046B
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
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                                                                                                                                            461
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TTCAAATTCCACATACTGAGAATGTGAAGCTTCTCTTTGCGATGGATTTGAGGAAATTAT
                               TTCAGCCTGGGGATGATGACTTTGTCGATGTTTGTCGAGAGTGGTTCGTCGAAAGTTG
                                                                     ATTTTTGTTCGTCCTTTGAAGTAGTGGCAGCATTGGTTTGGATAGCAAGGACAAAGGCTC
                                                                                                      ATTCTGGTCGACCGTATGTTTTCCTTCTTCCGATCGTTGAGGGACCGTTCCGAACCTCGA 436
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Pred. No. 0
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Pred. No.
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; TYPE: DNA
; ORGANISM: Taxus cuspidata
US-09-866-572A-21
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Sequence 19, Application US/09866572A
Patent No. US20020138859A1
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
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; DNA
; ORGANISM: Taxus cuspidata
US-09-866-572A-19
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                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
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                                                                                                                                                                                                                                                                              Sequence 21, Application US/09866572A Patent No. US20020138859A1 GENERAL INFORMATION:
                                                        SEQ ID NO 21
LENGTH: 911
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
                                                                                                                                                                            APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic
FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/866,572A
CURRENT FILING DATE: 2001-05-25
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Best Local Similarity
                                                                                                                PRIOR APPLICATION NUMBER: 09/457,046
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
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CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 09/457,046
                                                                                                 SOFTWARE: PatentIn Ver. 2.1
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RESULT 11
US-10-091-504-1271
US-10-091-504-1271
Sequence 1271, Application US/10091504
Publication No. US20030059908A1

GENERAL INFORMATION:

APPLICANT:

Rosen et al

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US-09-820-003A-3
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Best Local S
Matches 82
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APPLICANT: MERKULOV, Gennady et al.
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001196
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 3
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Best Local Similarity
Matches 116; Conserv
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                           30070 CCCAGGAGGCGGAGGTTGTGGTGAGTCGAGATCGCACCATTGCACTCCAGCCTGGGCAAC
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                    CTCTATTGAAGGCGTTAAAACCTTTGCGCTTTACCT 1964
                                                                     ACGAGTGACATCCAAAACTAACCCAAAAGACATAGAATGGCACAGTGGAGAAAACCCCTAT
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Pred. No.
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Pred. No. 7.7;
0; Mismatches 74;
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Sequence 1272, Application US/10091504
Publication No. US20030059908A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PC007C1
CURRENT APPLICATION NUMBER: US/10/091,504
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2442
                                                                                           RESULT 13
US-09-764-869-1271
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US-10-091-504-1272
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                                     GENERAL INFORMATION:
                                                      Sequence 1271, Application US/09764869 Patent No. US20020061521A1
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Best Local Similarity 53.0%;
Matches 80; Conservative
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Best Local
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CURRENT FILING DATE: 2002-03-07
 APPLICANT: Rosen et TITLE OF INVENTION:
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                     et al.
Nucleic Acids,
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Pred. No. 0.88; 
0; Mismatches 71;
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Proteins,
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1271
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; ORGANISM: Homo sapiens
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US-09-764-869-1272
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic acids, Proteins,
FILE REFERENCE: PC007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2442
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US-09-796-692-7801/c

Sequence 7801, Application US/09796692 Publication No. US20020198362A1 GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A.

APPLICANT:

Mannion, Jane

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PRIOR APPLICATION NUMBER: 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/22,903
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR FILING DATE: 2000-08-07
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7801
LENGTH: 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA; ORGANISM: Homo sapiens US-09-796-692-7801
Search completed: April Job time : 398 secs
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PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR PRIOR APPLICATION NUMBER: 60/200,799
PRIOR FILING DATE: 2000-04-28
PRIOR PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR APPLICATION NUMBER: 60/218,950
PRIOR APPLICATION NUMBER: 60/218,950
PRIOR APPLICATION NUMBER: 60/218,950
PRIOR APPLICATION NUMBER: 60/218,950
PRIOR APPLICATION NUMBER: 60/222,903
                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.6%;
Best Local Similarity 57.9%;
Matches 66; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
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        protein search, using sw model
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US-09-659-166-2
US-09-659-166-2
US-09-659-146-2
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US-09-157-420-1
US-09-644-922-2
US-09-844-922-5
US-09-844-922-7
US-09-844-970-16
US-09-8491-362-7
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US-09-184-001-2
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ALIGNMENTS	PCT-US92-03624-2	US-09-076-137-2	US-09-173-891-2	US-08-611-928-2	US-08-316-301A-2	US-08-304-626-2	US-08-158-232-2	US-08-063-170-2	US-07-675-772-2	US-07-876-280-2	PCT-US91-02321-6	US-08-431-333-6	US-08-429-998-6	US-07-668-648-6	US-09-718-810-2	US-09-718-841-2	US-08-746-682A-13	US-08-597-236-13	
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US-08-846-234-3
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                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
AMAE: NORMAN F. OBLON

REGISTRATION NUMBER: 24 618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-413-3000
TELEFAX: (703)-413-2220
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                        Query Match
Best Local S
Matches 14
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APPLICANT: OSUMI Chieko
APPLICANT: NOZAKI Jinshi
APPLICANT: NOZAKI Jinshi
APPLICANT: NOZAKI Jinshi
APPLICANT: NOZAKI Jinshi
APPLICANT: KIDA TAKAO
TITLE OF INVENTION: RAFFINOSE SYNTHASE GENE, METHOD FOR
TITLE OF INVENTION: PRODUCING RAFFINOSE, AND TRANSGENIC PL
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                       MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1755 S.
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
ZIP: 22202
                                                                        Local Similarity
les 14; Conserv
                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/846,234
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                  YDQDQMVVVQVPWP 14
YDQDQMVVVQVPWP
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                                                                        100.0%; ilarity 100.0%; Conservative (
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                                                                      Score 80; DB 4;
Pred. No. 5.4e-08;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #1.30 (EPO)
                                                                                                            Length 14;
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-846-234-5
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SOFTWARE: Fac
SOFTWARE: Fac
SEQ ID NO 21
FRIGHH: 404
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SEQUENCE CHARACTERISTICS:
LENGTH: 784 amino-
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                Sequence 21, Appl Patent No. 632331
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Best Local Similarity
                                                     CURRENT APPLICATION NUMBER: US/09/302,769
CURRENT FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 08/962,560
PRIOR FILING DATE: 1997-10-31
NUMBER OF SEQ ID NOS: 50
                                                                                                                                 APPLICANT: METCALF, Donald
APPLICANT: METCALF, Nicos A
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC AGENTS
FILE REFERENCE: 109762
                                                                                                                                                                                                                        APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (703)-413-3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/846,234
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: RAFFINOSE SYNTHASE GENE, TITLE OF INVENTION: PRODUCING RAFFINOSE, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KIDA Takao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         756 YDQDQMVVVQVPWP 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: NORMAN F. OBLON REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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                                        SEQ ID NOS: 50
PatentIn Ver. 2.0
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                                                                                                                                                                                                                     STARR, Robyn
NICHOLSON, Sandra E
                                                                                                                                                                                                                                                                                         ALEXANDER, Warren S
VINEY, Elizabeth M
                                                                                                                                                                                                                                                        WILLSON, Tracey A RICHARDSON, Rachael T
                                                                                                                                                                                                                                                                                                                                                                                  Application US/09302769
                                                                                                                                                                                                                                                                                                                              HILTON, Douglas J
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Best Local Similarity
Watches 7; Conserva
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; ORGANISM: Human
US-09-302-769-21
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US-08-802-466-2
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APPLICANT: TESTA, TANIA TAMSON
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30218
CURRENT APPLICATION NUMBER: US/09/659,166
CURRENT FILING DATE: 2000-09-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: UK 9
PRIOR FILING DATE: 1999-09-10
                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOTTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                        ZIP: 19406
COMPUTER READABLE FORM:
           ATTORNEY/AGENT INFORMATION: NAME: William T. Han
                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Creasy, et al TITLE OF INVENTION: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 YDDDQGSYVQVP 140
                                                                                            APPLICATION NUMBER: US/08/802 FILING DATE: 19 February 1997 CLASSIFICATION: 435
                                             FILING DATE
                                                                                                                                                                                                                                                                                          ADDRESSEE: Smilling ADDRESSEE: Smilling Swedeland
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NAME: William T. Ha
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                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                            STATE:
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                                                                                                                                                                                                            Diskette
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3ER: UK 9921505.5
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66.7%;
                                                                                                                              US/08/802,466
                                                                                                                                                                                                                                                                                                           Road
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Pred. No.
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                                                                                                        US-09-350-484-2
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US-09-350-484-2
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Patent NO. 6159716
GENERAL INFORMATION:
APPLICANT: Creasy, et al.
TITLE OF INVENTION: HUMAN PROTEIN KINASE HOACE72
                                                  Query Match
Best Local
                                  Matches
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                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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1 YDQDQMVVVQVP 12
                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                       NAME: William T. Han
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/802,466
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19406
COMPUTER READABLE FORM:
                                                                                                                   MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                  Similarity
8; Conserv
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                                                                                                                                                                                     TYPE: amino acids
                                                                                                                                                                     STRANDEDNESS: single
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TELEFAX: 610-270-4026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
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                                    Conservative
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                                                Score 38; DB
Pred. No. 79;
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                                  Mismatches
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US-09-157-420-1
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LENGTH: 1829
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6222095
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APPLICANT: MAKANISHI, Hiroyuki
APPLICANT: MANDAI, Kenji
APPLICANT: WADA, MANADU
APPLICANT: WADA, MANADU
APPLICANT: OBAISHI, Hiroshi
TITLE OF INVENTION: ACTIN FILAMENT-BINDING PROTEIN "L-AFADIN"
FILE REFERENCE: 98-1042*/LC(WMC)/653
CURRENT APPLICATION NUMBER: US/09/157,420
CURRENT FILING DATE: 1998-09-21
NUMBER OF SEQ ID NOS: 1
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                                                                TELEFAX: (415) 576-030 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA PATENTAL PATENTIA PPLICATION DATA:
APPLICATION NUMBER: US/09/064,922
FILING DATE: 22-APR-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1246 QDRMAPVQNQWP 1257
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Callis, Judy
APPLICANT: Worley, Cathy K.
TITLE OF INVENTION: Sequence
TITLE OF INVENTION: Product:
NUMBER OF SEQUENCES: 9
                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Laurence J.
REGISTRATION NUMBER: 35,551
REFERENCE/DOCKET NUMBER: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                              SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 YDDDQGSYVQVP 141
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TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                               ZIP:
                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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7; Conserv
                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                 California
                                                                                                                                                                                                                                                                                                                                                                                                                               Two Embarcadero Center, Eighth Floor
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                                                             5) 576-0300
) 576-0300
, NO: 2:
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                                                                                                                                       023070-085400US
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Pred. No. 3.4e+02;
Pred. No. 3.4e+02;
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Length 1829; Indels

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Version #1.30

for Degradation

Length 399; Indels

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Gaps

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US-09-491-362-7
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Best Local Similarity :
Tabes 7; Conservat
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           GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Lange, Bernd M
TITLE OF INVENTION: 1-DEOXY-D-XYLULOSE-5-PHOSPHATE REDUCTOISOMERASE, AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: WSUR14977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 58.0
                                                                                                                          Sequence 7, Application US/09491362 Patent No. 6281017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09064922 Patent No. 6222095
CURRENT APPLICATION NUMBER: US/09/491,362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09
FILING DATE: 22-APR-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Laurence J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Callis, Judy
APPLICANT: Worley, Cathy K.
TITLE OF INVENTION: Sequence
TITLE OF INVENTION: products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                    135 DGDWMLVGDVPW 146
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                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hyman, Laurence J. REGISTRATION NUMBER: 35,551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                      2 DQDQMVVVQVPW 13
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58.3%;
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                                                                                                                                                                                                                                                                                                           1; Mismatches
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Pred. No. 28;
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US-08-764-870-16
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Best Local Similarity
Thehes 6; Conserve
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; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-491-562-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Lange, Bernd M
TITLE OF INVENTION: 1-DEOXY-D-XYLULOSE-5-PHOSPHATE REDUCTOISOMERASE, AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: WSUR17549
CURRENT APPLICATION UNMBER: US/09/874,562
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/491,362
PRIOR APPLICATION NUMBER: 60/118,349
PRIOR APPLICATION NUMBER: 60/118,349
PRIOR FILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                       Sequence 16, Application US/08764870 Patent No. 6236946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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EARLIER APPLICATION NUMBER: 60/-
EARLIER FILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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TYPE: PRT
                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                APPLICANT: West, Brian
TITLE OF INVENTION: Nuclear Receptor
TITLE OF INVENTION: Binding Domains
                                                                                                                                                                             APPLICANT:
                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                          APPLICANT:
                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                 254 QDSSVLAQLGWP 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.28;
Local Similarity 50.08;
les 6; Conservation
                               ADDRESSEE: Cooley Godward STREET: Five Palo Alto Square,
                                                                                                                                                                                                                                                                                                                                                                                                                                  3 QDQMVVVQVPWP 14
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Palo Alto
: CA
                                                                                                                                                                           Fletterick, Robert J
Wagner, Richard L
Kushner, Peter J
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                                                                                                                                                          Apriletti, James W
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WMBER: 60/118,349
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                                                                                                                                                                                                                                                   Thomas S
                                                                                                                       Nuclear Receptor Ligands and Ligand
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Pred. No.
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                                   3000 El Camino Real
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85;
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Length 399;

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Gaps

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APPLICANT: NOTE: DESCRIPTION LIGANDS AND LIGAND BINDING DOMAINS FILE REFERENCE: UCAL-246/02US
FILE REFERENCE: UCAL-246/02US
CURRENT APPLICATION NUMBER: US/08/980,115
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: 08/764,870
EARLIER FILING DATE: 1996-12-13
EARLIER FILING DATE: 1995-12-14
EARLIER FILING DATE: 1995-12-14
EARLIER APPLICATION NUMBER: 60/008,543
EARLIER FILING DATE: 1995-12-13
EARLIER APPLICATION NUMBER: 60/008,543
EARLIER APPLICATION NUMBER: 60/008,543
EARLIER FILING DATE: 1995-12-13
SEARLIER FILING DATE: 1995-12-13
SEARLIER FILING DATE: 1995-12-13
SOFTMARE: PATENTING DATE: 1995-12-13
NUMBER OF SEQ ID NOS: 17
SOFTMARE: PATENTIN Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,540
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,543
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,606
APPLICATION NUMBER: US 60/008,606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 Amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: UC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/008,606
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: NAKAMULA, Jackie N
REGISTRATION NUMBER: 35,966
PROTESTINATION NUMBER: 35,966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265 DQMAVIQYSW 274
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Fletterick, Robert J.
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; OTHER INFORMATION: minimal ligand binding domain US-08-980-115-16
                                 ; ORGANISM: Mentha piperita US-09-874-562-2
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; Sequence 2, Applic

; Patent No. 6281017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δδ
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-09-874-562-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 2
LENGTH: 475
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Lange, Bernd M
TITLE OF INVENTION: 1-DEOXY-D-XYLULOSE-5-PHOSPHATE REDUCTOISOMERASE,
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: WSUR14977
                                                                                                NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Lange, Bernd M
TITLE OF INVENTION: 1-DEOXY-D-XYLULOSE-5-PHOSPHATE REDUCTOISOMERASE,
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: WSUR17549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09874562 Patent No. 6420159
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/874,562
CURRENT FILLING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/491,362
PRIOR FILING DATE: 2000-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 60/118,349 EARLIER FILING DATE: 1999-02-03 NUMBER OF SEQ ID NOS: 13
                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/118,349 PRIOR FILING DATE: 1999-02-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/491,362
CURRENT FILING DATE: 2000-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
                                                                  LENGTH: 475
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: DOMAIN
LOCATION: (184)..(437)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity hes 6; Conserv
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46.2%;
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Pred. No.
Score 37;
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Pred. No. le+02;
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DB 4;
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Length 475;
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Matches 6; Conservative 2; Mismatches 4; Indels 0; Caps 0;

Gy 3 DODMYVOYPHP 14

Db 331 DESTINATION 342

Search completed: March 27, 2003, 10:07:35

Job time: 4.41463 secs 7, 2003, 10:07:35
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Result
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Match
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188.389 Million cell updates/sec
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| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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Listing first 45 summaries
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  AAW53569
AAY17424
AAW57427
AAW57417
AAB98659
AAW57887
AAW57887
AAW578400
AAB93664
AAU67218
                                                                                                                                                                            SUMMARIES
Cucumber raffinose
Cucumber raffinose
Soybean protein: S
Soybean raffinose
Amino acid sequenc
Soybean raffinose
Herbicidally activ
Propionibacterium
                                                                                                                               Description
                                                                                                    Cucumber raffinose
                                                                                                                                                                                                                                                                                                                                                                    RESULT 1
AAW53569
ID AAW5
XX
  06-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                        AAW53569;
                                                                                                                                                                                                                                                                                                                                                                                AAW53569 standard; peptide; 14
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Arabidopsis thalia	AAG53160	21	692	52.5	
Human peptide enco	431	23	90	2	
Peptide #7535 enco	49	22	90	N	42
Peptide #6346 enco	AAM19912	22	90	2	
ma	AAM73298	22	90	Ņ	
n brain ex	AAM60626	22	90	2	42
#7392 e	S	22	90	Ν	
oocyte	AAR78233	16	863	ω	
rhg1 p120	AAM42231	22	877	5	
rhg1	AAM42229	22	877	ŗ	44
rhg1	AAM42227	22	877	5	
rhg1	AAM42221	22	877	ū	
rhg1 F	AAM42219	22	877	ŗ	
rhg1 p120	K)	22	854	S	44
1 16	AAM4 2230	22	854	5	
rhg1	AAM4 2228	22	854	5	44
rhg1	AAM42222	22	854	5	44
	AAM42220	22	854	ŗ	44
~	ABB10122	22	830	ŗ	44
Soybean raffinose	AAY70978	21	758	ŗ	44
S		21	673	5.	44
thali		21	637	5	44
is thali	AAG52085	21	535	5	44
idopsis	AAG07532	21	270	ū	44
is thali	AAG45845	21	269	5	44
is thali	84	21	229	5	44
	ω	21	229	5	44
11	œ	21	228	ŗ	
	0753	21	228	5	
finos	20	20	777	<u>5</u>	
sis thali	315	21	586	ა	
raffinos	20	20	572		45
thali	315	21	563	56.2	45
abidopsis th	531	21	484	σ.	45
Propionibacterium	982	22	148	.7	46

ALIGNMENTS

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The present sequence is a cucumber raffinose synthase fragment.
                                                                             Raffinose synthase gene 
transformed plant
                                                                                                                                      WPI; 1998-264858/24.
                                                                                                                                                                                                                  26-JUL-1996;
26-APR-1996;
                                                                                                                                                                                                                                                                                                                  07-APR-1998
                                                                                                                                                                                                                                                                                                                                                        JP10084973-A.
                                                                                                                                                                                                                                                                                                                                                                                             Cucumis sativus
                                                                                                                                                                                                                                                                                                                                                                                                                                  Cucumber; raffinose synthase; sucrose; galactinol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cucumber raffinose synthase residues 756 to 769.
                                      Example 2; Page 17; 26pp;
                                                                                                                                                                                                                                                                           28-APR-1997;
                                                                                                                                                                           (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                  96JP-0198079.
96JP-0107682.
                                                                                                                                                                                                                                                                           97JP-0111124
                                                                                                    ,
                                                                                               useful for preparation
                                      Japanese
                                                                                                 of.
                                                                                                 raffinose in
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RESULT 3
AAW53570
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AAY17424
    AC XX
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                          Query Match
Best Local :
                                                                                                                                  Matches
                                                                                                                                                                                                 The present invention describes a raffinose synthase, having an activity of forming raffinose from sucrose and galactinol. The raffinose synthase gene can be used for expression in a plant for the production of raffinose. The raffinose synthase can give raffinose from sucrose and galactinol efficiently. The present sequence represents a raffinose generates a contract the form currence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Raffinose synthase forms raffinose from sucrose and galactinol, has an optimum pH of 6 to 8 and working temperature of 35 to 40 degrees C, has a molecular weight of 75 to 95 kDa by gel filtration or 90 to 100 kDa by PAGE and SDS-PAGE under reductive conditions and is inhibited by iodoacetamide, N-ethylmaleimide and myoinositol.
    06-JUL-1998
                       AAW53570;
                                         AAW53570 standard;
                                                                                                                                                                        Sequence
                                                                                                                                                                                          synthase peptide from
                                                                                                                                                                                                                                                                                   sucrose and
                                                                                                                                                                                                                                                                                                                                                                                                               JP11123080-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Cucumis sativus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cucumber raffinose synthase peptide SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY17424 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                             Example 2; Page 22; 37pp; Japanese.
                                                                                                                                                                                                                                                                                 New raffinose synthase gene - sucrose and galactinol
                                                                                                                                                                                                                                                                                                                WPI; 1999-340516/29.
                                                                                                                                                                                                                                                                                                                                                      24-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                             11-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                   (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                                                                                                                                                                         24-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Raffinose synthase;
                                                                                            _
                                                                                                                                          Local Similarity
                                                                                                             1 YDQDQMVVVQVPWP 14
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                                                                                            YDQDQMVVVQVPWP 14
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                                                                                                                                  14;
                                                                                                                                                                         14 AA;
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                                                                                                                                  Conservative
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   (first entry)
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                                                                                                                                                                                                                                                                                                                                                      97JP-0292969
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                                          Protein;
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                                                                                                                                                                                           cucumber.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      galactinol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 80; DB
Pred. No. 1.7
D; Mismatches
                                                                                                                                          Score 80; DB 20;
Pred. No. 1.7e-07;
                                                                                                                                                                                                                                                                                          for production of raffinose from
                                          B
                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; DB 19;
. 1.7e-07;
ches 0;
                                                                                                                                                    Length 14;
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                                                                                                                                  Indels
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                                                                                                                                                                                                                                 synthase
                                                                                                                                 0;
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AAY17417
ID AAY1
    PR XX PA DR DR PT PT
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PR
XX
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Best Local S
Matches 14
New raffinose synthase gene - sucrose and galactinol
                               WPI; 1999-340516/29
N-PSDB; AAX61238.
                                                                                                                                                              Cucumis sativus
                                                                                                                                                                                                    Cucumber raffinose
                                                                                                                                                                                                                                            AAY17417;
                                                                                24-OCT-1997;
                                                                                                    24-OCT-1997;
                                                                                                                       11-MAY-1999.
                                                                                                                                          JP11123080-A.
                                                                                                                                                                                                                        29-JUL-1999
                                                                                                                                                                                                                                                              AAY17417 standard;
                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAV22250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUL-1996;
26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP10084973-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cucumber;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cucumber raffinose synthase
                                                            (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transformed plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-264858/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cucumis sativus
                                                                                                                                                                                                                                                                                                               756 YDQDQMVVVQVPWP
                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                 1 YDQDQMVVVQVPWP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             raffinose
                                                                                                                                                                                                                                                                                                                                                                                           784 AA;
                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                       (first entry)
                                                                                97JP-0292969
                                                                                                    97JP-0292969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96JP-0198079
96JP-0107682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97JP-0111124
                                                                                                                                                                                                   synthase
                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            synthase;
                                                                                                                                                                                                                                                                                                                                                              100.
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€1 6,2 1

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6 to 8 and working temperature of 35 to 40 degrees C, has a molecular weight of 75 to 95 kDa by gel filtration or 90 to 100 kDa by PAGE and SDS-PAGE under reductive conditions and is inhibited by iodoacetamide, N-ethylmaleimide and myolnositol.
                                                                                                                                                                                                                                                                                                                                                                                          Raffinose synthase; sucrose; galactinol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is cucumber raffinose synthase, forms raffinose from sucrose and galactinol, has an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Pages 17-20; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raffinose synthase gene - useful for preparation of raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 80; DB
Pred. No. 1.5
); Mismatches
for production of raffinose from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sucrose;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 19;
1.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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RESULT 5
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                                           Query Match
Best Local S
Matches 8
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Best Local S
Matches 14
                                                                                                                         The present invention relates to a mutant protein of raffinose synthase in which at least one aromatic acid present at the position of about 1-7 amino acids from the N-terminus is deleted or replaced. The mutant protein can be used for reducing the raffinose oligosaccharide content in a plant body. The present protein from soybean, was used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of forming raffinose from sucrose and galactinol. The raffinose synthase gene can be used for expression in a plant for the production of raffinose. The raffinose synthase can give raffinose from sucrose and galactinol efficiently. The present sequence represents raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2;
                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                  09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                        03-JUL-2000; 2000JP-0200571.
                                                                                                                                                                                                                                                                                                                                                                                       JP2001078783-A
                                                                                                                                                                                                                                                                                                                                                                                                           Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                  \begin{tabular}{ll} \textbf{Mutant: mutein: raffinose synthase: raffinose oligosaccharide reduction: plant: soybean. \end{tabular}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB98659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB98659 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthase from cucumber.
                                                                                                                                                                                                                     Novel mutant protein of raffinose synthase is useful for raffinose oligosaccharide content in a plant body -
                                                                                                                                                                                                                                                         WPI; 2001-313373/33.
N-PSDB; AAH27438.
                                                                                                                                                                                                                                                                                                                                                              27-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soybean protein: SEQ ID 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention
                                                                                                                                                                                                                                                                                          (SUMO ) SUMITOMO CHEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   756
 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                       3 QDQMVVVQVPWP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YDQDQMVVVQVPWP 14
                                                                                                                  present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YDQDQMVVVQVPWP 769
EDKMLRVQVPWP 768
                                             8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 25-27; 37pp; Japanese.
                                                                                           780 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              784 AA;
                                                                                                                                                                                                Page 18-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                  99JP-0196036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein;
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                                                        662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              describes a raffinose synthase, having an activity
                                                                                                                                                                                                                                                                                           CO LTD
                                                                                                                                                                                             30pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          780
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Pred.
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Pred. No. 1.5
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                                             Mismatches
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. 1.5e-05;
ches 0;
                                                      DB 22;
2.9;
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RESULT

10-AUG-1999

JP11215984-A.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the soybean raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gastrointestinal flora; soybean.
                                                                                                             Glycine max.
                                                                                                                                                                                                                                                                                                                                         AAY30143;
                                                                                                                                                                                                                                                                                                                                                                                                 AAY30143 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAV40801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soybean raffinose synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-SEP-1998
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                                                                                                                                                                Raffinose synthase; plant; sucrose;
                                                                                                                                                                                                                        Amino acid sequence of a raffinose synthase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP849359-A2
                                                                                                                                                                                                                                                                                   26-0CT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity les 8; Conserv
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                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                 Protein; 781 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 50;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N
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Matches 8
 Query Match
                   Sequence
                                   properties
                                              the
                                                                        Example 6;
                                                                                                                        N-PSDB;
                                                                                                                                WPI; 2001-104537/12
                                                                                                                                                                                       30-APR-1999;
01-SEP-1999;
                                                                                                                                                                                                                                                                                                                              07-MAR-2001
                                                                                                                                                                                                                                                                                                                                                AAB49400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a raffinose synthase protein. The sequence is isolated from plant material. The protein forms raffinose by complexing alpha(1 to 6)- D-galactosyl hydroxyl group of the 6C of D-glucose residue in sucrose molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; Page 25-27; 40pp; Japanese.
                                                                                                    New soybean plant promoters useful for
                                                                                                                                                                                                                 27-APR-2000;
                                                                                                                                                                                                                                   02-NOV-2000
                                                                                                                                                                                                                                                      EP1048733-A2
                                                                                                                                                                                                                                                                                         Plant promoter; transgenic
                                                                                                                                                                                                                                                                                                           Soybean raffinose synthase
                                                                                                                                                                                                                                                                                                                                                                 AAB49400 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                   (SUMO ) SUMITOMO CHEM CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-NOV-1997;
18-DEC-1996;
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nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                        3 QDQMVVVQVPWP 14
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                                           present invention provides novel plant promoters which can be used production of transgenic plants which express genes with desired % \left( 1\right) =\left\{ 1\right\} 
                                                                                            desired
                                                                                                                                                                                                                                                                                                                                                                                                               EDKMLRVQVPWP 769
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DB; AAZ10002.
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                                                                                                                        AAC89523.
                                                                        Page 24-27;
                                                                                                                                                  Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      781 AA;
                   781
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                                                                                            properties
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99JP-0247211.
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96JP-0338673.
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                                                                                                                                                                                                                                                                                                                                                                 Protein;
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60
62.5%;
                                                                       36pp; English
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                                                                                                                                                                                                                                                                                         plant;
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Pred.
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Score
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                                                                                                                                                                                                                                                                                       desired property.
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50;
                                                                                                 generating transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
2.9;
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Length 781;
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RESULT 10
AAU67218
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ABB93664
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Best Local :
                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                    The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant
Propionibacterium acnes immunogenic protein #28114
                          27-FEB-2002
                                                 AAU67218;
                                                                         AAU67218 standard;
                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                       Claim 5; SEQ ID NO 2875; 261pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                organisms
                                                                                                                                                                                                                                                                                                                                                                                                          Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                    are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-269010/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tietjen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB93664 standard; Protein;
                                                                                                                                                                                                                                                      useful as
                                                                                                                                                                                                                                                                              sequences are selected.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-AUG-2001; 2001WO-EP09892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200210210-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Herbicidal; plant; agriculture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Herbicidally active polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAY-2002
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                                                                                                                                                         3 QDQMVVVQVPW 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             herbicides
                                                                                                                                                                                                                                                                are selected. The polypeptides or nucleic acids encoding them for identifying modulators. The identified modulators are
                                                                                                                                                                                                                               783 AA;
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                                                                                                                                                                                  Conservative
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                          (first entry)
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                                                                         Protein;
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72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID NO
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                                                                                                                                          RESULT 11
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P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
P. acnes is also involved in infections of bone, joints and the central
nervous system, however it is particularly involved in the inflammatory
lesions associated with acne vulgaris. A method for detecting the
presence or absence of P. acnes in a patient comprises contacting a
sample with a binding agent that binds to the proteins of the invention
and determining the amount of bound protein in the sample. The
polypeptides may be used as antigens in the production of antibodies
specific for P. acnes proteins. These antibodies can be used to
downregulate expression and activity of P. acnes polypeptides and
therefore treat P. acnes infections. The antibodies may also be used as
diagnostic agents for determining P. acnes presence, for example, by
converse in the sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; EIISA; inflammatory leaion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
Propionibacterium acnes immunogenic protein #10721
                                    27-FEB-2002
                                                                      AAU49825
                                                                                                         AAU49825 standard; Protein; 148
                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID No 28413; 1069pp; English.
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02-JUN-2000; 2000US-208841P
07-JUL-2000; 2000US-216747P
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nes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                           98 AA;
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                                   (first entry)
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77.8%;
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, Jen S, Carter
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18-OCT-2000

(first entry)

Arabidopsis thaliana protein fragment SEQ ID NO: 67650

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RESULT 12
AAG53157
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CC Note: The sequence data for this patent did not form part of the printed constitution but uses obtained in alectroid forms at directly from vittod.
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AAG53157 standard; Protein; 484
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specification, but was obtained in electronic
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uve J, Zhang Y,
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2000US-208841P.
2000US-216747P.
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77.8%;
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, Jen S, Carter D;
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Protein identification; hybridisation assay; ge termination sequence. Arabidopsis thaliana. Ep1033405-A2. 06-SEP-2000; 2000EP-030 25-FEB-1999; 99US-012 25-MAR-1999; 99US-012 27-MAR-1999; 99US-012 27-MAR-1999; 99US-012 28-APR-1999; 99US-012 29-MAR-1999; 99US-012 21-APR-1999; 99US-012 21-APR-1999; 99US-013
nlification; signal transduction pathway; metabolic pathway; sequence. sequence. thaliana. 2. 2000EP-0301439. 299US-0121855 299US-0121865 299US-0125788 299US-0126745 299US-012674
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23-JUN-1999 23-JUN-1999 23-JUN-1999 23-JUN-1999 30-JUN-1999 30-JUN
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RESULT 13
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29-SEP-1999
11-OCT-1999
                                                                                                                               AAG53156 standard;
                                     Protein identification; signal transduction pathway; metabolic pathway; hybridiantion assay; genetic mapping; gene expression control; promoter;
                                                                    Arabidopsis
          Arabidopsis thaliana
                               termination
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                              sequence.
                                                                    thaliana protein fragment SEQ
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99US-0153070.
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RESULT 14
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AC AAY32075;
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                     /note= "encoded by 144
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                                                                                        Arabidopsis thaliana.
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L_change 20-Jun-2000 H.; Dean, C.; Bergkamp, R.; D T.; Pohl, T.M.; Terryh, N.; G ar, M.; Schaeffer, M.; Funk, B Lfort, A.; Pons, A.; Pulgdomen , K.; Benes, V.; Rechman, S.; chromosome 4 of Arabidopsis t	ein IAA14 #text_change 20-Aug-1999 #text_change 20-Aug-1999 AAC49055.1; PID:g972931 AAC49055.1; PID:g972931 Length 164; Length 164; 4; Indels 0; Gaps 0;	conserved hypothet yeck protein - Esc hypothetical prote hypothetical prote pectinesterase (EC hypothetical prote glutamate-ammonia probable beta-1,3-conserved hypothetical prote hypothetical prote hypothetical prote hypothetical prote probable reverse t s-afadin - rat phosphodiesterase exoribonuclease, v

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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 24-Aug-2001
                                 A; Map position:
C; Superfamily:
                                                                                                                A; Molecule type: DNA
A; Residues: 1-234 <STO>
                                                                                                                                                                          R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprir Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
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A;Cross-references: GB:Z97336; NID:g2244788; PIDN:CAB10234.1; PID:g2244811
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                                                                                               A;Cross-references: GB:NC_001268; NID:g5302771; PIDN:CAB46059.1; GSPDB:GN00140
                                                                                                                                              A; Status: preliminary
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A; Residues: 1-229 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE005172; NID:g4389514; PIDN:AAB70451.2; GSPDB:GN00141
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                                                                                Genetics:
   Query Match
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les 8; Conser
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                               auxin-induced protein aux28
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Pred. No.
 Score 44;
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Pred. No.
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alo Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim C.A.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                               A;Note: F18021.60
C;Superfamily: unassigned Ser/Thr
                                                                                                                                                                                                                                                   A; Experimental source: cultivar Columbia; BAC clone F18021 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                    A; Reference number: Z24474
A; Accession: T47727
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F18021.60 - Arabidopsis thaliana (;Speciles: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000 C;Accession: T47727
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T47727
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C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C;Accession: C86467
                                                                                                                                                                                                      A; Map position: 3
A; Introns: 244/2; 491/1; 511/1
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A; Residues: 1-719 <BEN>
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C;Genetics:
A;Map position: 1
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A; Residues: 1-619 <STO>
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Matches 8; Conservative
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QGQVIVIQLPW 110
                                      QDQMVVVQVPW 13
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                                                                                                Score 44;
Pred. No.
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l; Mismatches
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No.
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C;Accession: T52251
R;Gao, Y.; Schofield, O.M.; Leustek, T.
Plant Physiol. 123, 1087-1096, 2000
A;Title: Characterization of sulfate assimilation
A;Reference number: Z26003; MUID:20349720; PMID:1(
                                                                                                        5'-adenylylsulfate reductase (EC 1.8.99.-) [validated] - green alga (Enteromorpha C;Species: Enteromorpha intestinalis (hollow green seaweed)
C;Date: 20-Oct_2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
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A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gc
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A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrol A;Reference number: A97359; PMID:11743194
A;Accession: G97360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-418 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL41046.1; PID:g17738332; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: The Genome of the Natural Genetic A; Reference number: AB2577; PMID:11743193 A; Accession: AH2578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              intracellular PHB depolymerase [imported] - Agrobacterium tumefaciens (strain C58, C;Species: Agrobacterium tumefaciens C;Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-418 < KUR>
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C;Accession: G97360
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7; Conser
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Rickettsia prowazekii hypothetical protein RP681
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87.5%;
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Pred. No. 8.8;
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    PMID:10889258
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; Markelz,
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rkelz, B.
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FDRQQLVTTEIQWP

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F: 45-86 //Product: VLDL receptor #status predicted <ARTY
F: 45-78 //Domain: Extracellular #status predicted <EXTY
F: 45-78 //Domain: LDL receptor ligand-binding repeat homology <LDL1>
F: 90-126 //Domain: LDL receptor ligand-binding repeat homology <LDL2>
F: 131-167 //Domain: LDL receptor ligand-binding repeat homology <LDL3>
F: 131-27 //Domain: LDL receptor ligand-binding repeat homology <LDL4>
F: 211-247 //Domain: LDL receptor ligand-binding repeat homology <LDL5>
F: 257-291 //Domain: LDL receptor ligand-binding repeat homology <LDL6>
F: 257-391 //Domain: LDL receptor ligand-binding repeat homology <LDL6>
F: 263-37 //Domain: LDL receptor ligand-binding repeat homology <LDL7>
F: 316-37 //Domain: LDL receptor ligand-binding repeat homology <LDL8>
F: 378-412 //Domain: EGF homology <EG1>
F: 418-452 //Domain: EGF homology <EG2>
F: 499-544 //Domain: LDL receptor YWTD-containing repeat homology <YW3>
F: 499-544 //Domain: LDL receptor YWTD-containing repeat homology <YW3>
F: 586-531 //Domain: LDL receptor YWTD-containing repeat homology <YW4>
F: 675-71 //Domain: LDL receptor YWTD-containing repeat homology <YW6>
F: 675-71 //Domain: LDL receptor YWTD-containing repeat homology <YW6>
F: 675-71 //Domain: LDL receptor YWTD-containing repeat homology <YW6>
F: 675-71 //Domain: LDL receptor YWTD-containing repeat homology <YW6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:x80207; NID:g609265; PIDN:CAA56505.1; PID:g609266
C;Comment: This receptor mediates uptake of very low density lipoprotein and vitellog
C;Comment: There is some evidence for the existence of a longer splice form containin
C;Superfamily: LDL receptor; EGF homology; LDL receptor ligand-binding repeat homolog
C;Keywords: duplication; fatty acid metabolism; glycoprotein; receptor; transmembrane
C;Superfamily: LDL receptor; EGF homology; LDL receptor ligand-binding repeat homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: S51789; MUID:95045409; A; Accession: S51789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLDL receptor precursor - chicken

N;Alternate names: very low density lipoprotein receptor; vitellogenin receptor
C;Species: [Gallus gallus (chicken)
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
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δÃ
                                                                                                                                                                                                                            F;824-828/Region:
F;169,773/Binding
                                                                                                                                                                                                                                                                                        F;788-809/Domain:
                                                                                                                                                                                                                                                                                                                      F;726-769/Domain:
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A; Residues: 1-863 <BUJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Bujo, H.; Hermann, M.; Kaderli, M.O.; Jacobsen, L.; Sugawara, S.; Nimpf, J.; EMBO J. 13, 5165-5175, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: $51789
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A; Residues: 1-423 <GAO>
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A; Status: pre
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                                                                 Matches
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                                                                                               Local
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   1 YDQDQMVVVQVPWP 14
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                                                              Similarity 5; Conserv
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                                                                 Conservative
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                                                                                                                                                                                        transmembrane #status predicted <TMM>
coated-pit mediated internalization signal
site: carbohydrate (Asn) (covalent) #status predicted
site: carbohydrate (Asn) (covalent) #status predicted
,400-412,418-428,424-437,439-452,726-739,735-754,756-769/Disulfide
                                                                                                                                                                                                                                                                                                                      EGF homology <EG3>
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                                                                                            53.8%;
                                                                                            Score 43;
Pred. No.
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Pred. No. 8
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                                                                 Mismatches
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                                                                                         DB 20;
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                                                                 Gaps
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C;Genetics:
A;Gene: 40
A;Gene: 40
C;Superfamily: varicella-zoster virus gene 38 protein
                       R:Theologis, A.; Ecker, J.R.; Palm, Chin, C.W.; Chung, M.K.; Conn, L.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
                                                                                                                                             probable auxin response factor, 53188-50111 [imported] - Arabidopsis thalia
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F7A19.18 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001 C;Accession: D86274 R;Theologis; A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Arabidopsis, B.; Hulzar, L. ansen, N.F.; Hughes, B.; Hulzar, L. Nature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Reference and analysis of chromosome l of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tegument protein 40 - equine herpesvirus 4 (strain NS80567)
C;Species: equine herpesvirus 4
A;Variety: strain NS80567
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C;Accession: T42584
R;Telford, E.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.
                                                                                                                                                                                                                                 C86468
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Best Local Similarity
"~+~hes 6; Conserv?
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                                                                                                                           C; Accession: C86468
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A; Residues: 1-529 <TEL>
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A; Residues: 1-500 <STO>
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Best Local Similarity
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50.0%;
  Jenkins,
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45.5%;
J.;
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Pred. No.
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Pred. No.
                                                                    C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alo Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Johnson-Hopson,
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. 16;
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C.;
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                                                                                                                                                                                                    Arabidopsis thaliana
Khan,
s.;
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Khaykin,
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                                                                         Alonso,
war, K.,
  Kim,
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A; Molecule type: DNA
A; Residues: 1-530 <TEL>
A; Cross-references: GB: M86664; NID: g330791;
                                                                                                                                                    gene 40 protein - equine herpesvirus 1 (strain Ab4p) C;Species: equine herpesvirus 1 A;Note: host Equus caballus (domestic horse) A;Note: 30-Sep-1992 #sequence_revision 30-Sep-1992 #C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #S;Telford, E.A.R.; Watson, M.S.; McBride, K.; Daviso submitted to GenBank, March 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; Wh Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Kowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; S Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Wunter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                               A; Reference number: A36805
A; Accession: F36799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
A; Map position: 1
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                                                                                                                                 A; Description: The DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C:Genetics:
A;Gene: F1504.37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein F1504.37 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-767 <STO>
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A; Residues: 1-600 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: G86476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE005172; NID:g10092376; PIDN:AAG12783.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
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                                                                                                                               herpesvirus-1
     PIDN:AAB02476.1; PID:g330833
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Maiti, R.; Ma
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R:Telford, E.A.R.: Mctson, M.S.: McBride, K.; Davison, A.J.
VICOLOgy 189, 304-316, 1992
A:Title: The DNA sequence of equine herpsyltus-1.
A:Reference number: A4181; MUD1922556; PMID:3138606
A:Contents: embotation; passible protein-coding frames
C:Gonetinelibre anino acid nor nucleotical sequence 1s given
C:Superfamily: varicella-zoster virus gene 38 protein
Ouery Match
Dasi: Local Similarity
D3:A%; Score 41; Db1; Length 530;
Best Local Similarity
D4:A; Pred. No. 26;
Matches 4; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
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Search completed: March 27, 2003, 10:06:52
Job time: 6.0172 secs
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   protein search, using sw
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P93830 arabidopsis
P98165 gallus gall
Q9x178 arabidopsis
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ALIGNMENTS

STRAIN=cv. Columbia;	RC :
SECTION PARTY NAME OF THE PART	χ : 0 :
Nature 408:816-820(2000).	2 Z
na.";	RT
"Sequence and analysis of chromosome 1 of the plant Arabidopsis	RT
	RA
Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,	RA
, Tallon L.J., Tambunga G., Toriumi M.J., Tor	RA
H., Salzberg S.L., Schwartz J.R., Shinn P., Southwic	RA
Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,	RA
Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,	RA
Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,	RA
Langin-Hooper S., Lee A. Lee J.M. Lenz C.A. Li J.H. Li Y.P.	RA
Kim C.J. Koo H.L. Kremenetskala I Kurtz D.B. Kwan A. Lam B.	RA
S. Khaykin E.	RA
Gill J.E. Goldsmith A.D. Hansen R. Hughes R. Hujzar I.	RA :
Dunn D. Efau D. Feldblyum T. V. Feng T. D. Fong B. Fidif C v.	R S
Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,	U 7
White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,	RA
Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,	RA
	RX
STRAIN=cv. Columbia;	RC
SEQUENCE FROM N.A.	RP
[3]	RN
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ROUSE D., Mackay P., Stirnberg P., Estelle M., Levser O.:	RA
MEDLINE-98146427; PubMed-9478901;	RX
STRAIN-OV COlumbia:	R ;
LEU-16. ASD-118 AND PRO-121	공 전 건
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Proc Nath Acad Sci N S A 04.11786-11701/1001	8 2
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Matches
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       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Very low-density lipoprotein receptor precursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced |
SSP consortium (Salk/Stanford/PEGC).";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COULD ACT AS REGULATOR OF GENES RESPONSIBLE FOR
MEDIATING THE VARIOUS AUXIN-INDUCED EVENTS RESPONSIBLE FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Theologis A.; "Full Length cDNA of gene F19P19.31 (GI:4389514)."; "ibmitted (JAN-2001) to the EMBL/GenBank/DDBJ datab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Toriumi M.J., Yu G., Brooks S.Y., Chao Chen H., Karlin-Neumann G., Kim C.J., Lam B., Miranda M., Nguyen Palm C.J., Shinn P., Southwick A.M., Davis R.W., Ecker J.R.,
(Vitellogenin
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Shinozaki K., Davis R.W.,
                                                              LDVR_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDUCTION: BY AUXIN.

INDUCTION: BY AUXIN.

MISCELLANEOUS: Increased auxin response of mutants axr3-1 and miscellaneous: form an increased stability of AXR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        axr3-3 may result form an increased stabil SIMILARITY: BELONGS TO THE AUX/IAA FAMILY.
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SUBCELLULAR LOCATION: Nuclear.
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SUBUNIT: Homo and heterodimers.
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                                                                                                                                                                                                                                                                                                            2309; AUX_IAA; 1.
family; Nuclear protein;
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                                                                                                                                                                                                                ASSOCIATED WITH L-88.

SUPPRESSES THE AXR3-1 PHENOTYPE,
ASSOCIATED WITH L-88.
                                                                                                                                                                                                                                              : SUPPRESSES THE AXR3-1 PHENOTYPE, ASSOCIATED WITH L-88.
: SUPPRESSES THE AXR3-1 PHENOTYPE;
                                                                                                                                                                                                                                                                                        IN AXR3-3; INCREASES
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PROSITE; PS00010; PROSITE; PS00022; PROSITE; PS01186; PROSITE; PS01187; PROSITE; PS01209; PROSITE; PS50068;
                                             DOMAIN
TRANSMEM
  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00261; LDLRECEPTOR. SMART; SM00179; EGF_CA; 2. SMART; SM00001; EGF_like; 1. SMART; SM000192; LDLa; 8. SMART; SM00135; LY; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                            CHAIN
                                                                                                                    SIGNAL
                                                                                                                                                            Endocytosis;
                                                                                                                                                                                      Glycoprotein; VLDL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00057; ldl_recept_a; Pfam; PF00058; ldl_recept_b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X80207; CAA56505.1; HSSP; P01130; 1AJJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barber D.L., Sanders E.J., Aebersold R., Schneider W.J "The receptor for yolk lipoprotein deposition in the cl J. Biol. Chem. 266:18761-18770(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nimpf J., Yamamoto T., Schneider W.J.; "Chicken occyte growth is mediated by an eight ligand binding repeat member of the LDL receptor family."; EMBO J. 13:5165-5175(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bujo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002172; LDL_recept_A.
InterPro; IPR000033; Ldl_receptor_rep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=White leghorn; TISSUE=Foll MEDLINE=92011638; PubMed=1655760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=White leghorn; TISSUE=Ovary; MEDLINE=95045409; PubMed=7957081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 510-518; 546-554 AND 819-827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLDLR OR VTGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity).

SIMICELLULAR LOCATION: Type I multi-
SUBCELLULAR LOCATION: Type I multi-
TISSUE SPECIFICITY: ABUNDANT II
TISSUE SPECIFICITY: ABUNDANT II
SKELETAL MUSCLE.

SKELETAL MUSCLE.
SIMILARITY: CONTAINS 8 LDL-REC
SIMILARITY: CONTAINS 3 EGF-LIK

SIMILARITY: CONTAINS 3 EGF-LIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Binds VLDL and transports it into cells by endocytosis. In order to be internalized, the receptor-ligand complexes must first cluster into clathrin-coated pits. Binding to Reelin induce tyrosine phosphorylation of Dabl and modulation of Tau phosphorylation (By similarity).

SUBUNIT: Binds to the extracellular matrix protein Reelin (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
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                                                                       domain;
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44
44
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IPR000561; EGF-like.
IPR001881; EGF_Ca.
  786
810
49
                                                                                                                                                          Coated pits;
Repeat.
43
863
785
809
863
87
                                                                                                                                                                                                       ASX_HYDROXYL; 2.; ASX_HYDROXYL; 2.; EGF_1; FALSE_NEG.; EGF_2; 3.; EGF_CA; 2.; LDLRA_1; 8.; LDLRA_2; 8.
                                                                                                                                                                                      Cholesterol metabolism; Lipid
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                                             EXTRACELLULAR POTENTIAL.
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IN OOCYTES; MUCH LESS
                                                                                            LOW-DENSITY LIPOPROTEIN RECEPTOR
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                                                                                                                                                               Receptor;
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                                                                                                                                                                                    transport;
                                                                                                                                                               Signal;
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FUT8_AF
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       FUT8_ARATH STANDARD;
Q9X178;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last seque)
15-JUN-2002 (Rel. 41, Last annot)
Probable fucosyltransferase 8 (Probable fucosyltransferase 8)
FUT8 OR AT1G14100 OR F7A19.18.
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(Mouse-ear
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ferase 8 (EC 2.4.1.-) (A
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LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 5.
LDL-RECEPTOR CLASS A 5.
LDL-RECEPTOR CLASS A 6.
LDL-RECEPTOR CLASS A 6.
LDL-RECEPTOR CLASS A 8.
LDL-RECEPTOR CLASS A 8.
LDL-RECEPTOR CLASS B 2.
LDL-RECEPTOR CLASS B 2.
LDL-RECEPTOR CLASS B 3.
LDL-RECEPTOR CLASS B 3.
LDL-RECEPTOR CLASS B 4.
LDL-RECEPTOR CLASS B 5.
LDL-RECEPTOR CLASS B 6.
EGF-LIKE 3.
ENDOCYTOSIS SIGNAL (POTENTIAL).
BY SIMILARITY.
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01-DEC-1992 (Rel. 2
01-DEC-1992 (Rel. 2
01-DEC-1992 (Rel. 2
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Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheu R. F., Chin C.W.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheu R.F., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Kim C.J., Koo H.L., Kremenetskala I., Kuriz D.B., Kwan A., Lam B.,

RA Kim C.J., Koo H.L., Kremenetskala I., Kuriz D.B., Kwan A., Lam B.,

RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

Tsequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; r. Transferase; GLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21608393; PubMed=11743104; Sarria R., Wagner T.A., O'Neill M.A. "-''
Keegstra K., Raikhel N '''
"Character"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21016719; PubMed=11130712;
Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Ke White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004938; XG_FTase.
Pfam; PF03254; XG_FTase; 1.
Transferase; Glycosyltransferase; Golgi stack; C
SEQUENCE 500 AA; 57538 MW; 1C5BB6152BFAE690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Characterization of a family of Arabidopsis
"Characterization of a family of Arabidopsis
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STRAIN-CV. Columbia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AC007576; AAD39294.1; -.
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Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Chung M.K., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y., Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L., Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E., Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B., Langin-Hooper S., Lee A., Lee J.M., Lear C.A., Li J.H., Li Y.-P., Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Abel S., Nguyen M.D., Theologis A., "The PS-IAA4/5-like family of early Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=cv. Columbia;
MEDLINE=95387393; PubMed=7658471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no rest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=cv. Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.
Equine herpesvirus type 1 (strain Ab4p) (EHV-1).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21016719; PubMed=11130712;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92295566; PubMed=1318606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Pfam; PF03252; UL21; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEIILIEEPWP 294
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Palm C.J., Shi
Theologis A.,
                                                                                                          Sugiura M., Tabata S.;
Sequence analysis of the genome of
Synechocystis sp. strain PCC6803. I.
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Justinocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome."

DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                 MEDLINE=96127529; PubMed=8590279; MEDLINE=96127529; PubMed=8590279; Medline=96127529; Medline=96127529
                                                                                                                                                                                                                                                                                                                                                                                                                                             Synechocystis sp. (strain Bacteria; (yanobacteria; )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activating enzyme).
ACS OR SLL0542.
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30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Acetyl-coenzyme A synthetase (EC 6.2.1.1) (Acetate--CoA ligase) (Acyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Multigene family; Nuclear protein; Translation regulation CONFLICT 34 34 K -> N (IN REF. 1). SEQUENCE 189 AA; 21031 MW; 5E9B130584A75465 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: COULD ACT AS REGULATOR OF GENES RESPONSIBLE FOR MEDIATING THE VARIOUS AUXIN-INDUCED EVENTS RESPONSIBLE FO
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SIMILARITY: BELONGS TO THE AUX/IAA FAMILY.
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Mismatches
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HSSP; P08659; 1LCI.
InterPro; IPR000873; AMP-bind.
Pfom; PF00501; AMP-binding; 1.
PRINTS; PR00154; AMPBINDING.
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SEQUENCE 653 AA; 73052 MW; 5EBC
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P16688;
01-AUG-1990
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16-OCT-2001
PhnJ protein
Chen C.-M., Ye Q.-Z., Zhu Z., Wanner B.L., Walsh C.T.;

"Molecular biology of carbon-phosphorus bond cleavage. Cloning a sequencing of the phn (psil) genes involved in alkylphosphonate uptake and C-P Lyase activity in Escherichia coli B.";

J. Blol. Chem. 265:461-4471(1990).

-I- FUNCTION: BELONGS TO AN OPERON INVOLVED IN ALKYLPHOSPHONATE UPTAKE AND C-P LYASE. EXACT FUNCTION NOT KNOWN.

-I- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF STRAIN K12.
                                                                                                                                                                                                                                                                             STRAIN-K12 / MG1655;
MEDLINE-95334362; PubMed-7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Da
Blattner F.R.;
"Analysis of the Escherichia coli genome VI:
region from 92.8 through 100 minutes.";
Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-91193228; PubMed-1840580; Makino K., Kim S.K., Shinagawa H., Amemura M., Nakata Makino K. analysis of the cryptic and functional phn phosphonate use in Escherichia coli K-12."; J. Bacteriol. 173:2665-2672(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PIR; B35719; B35719.
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ECOGene; EG10719; phnJ.
Alkylphosphonate uptake; Complete proteome.
Alkylphosphonate uptake; Complete STRAIN B).
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V -> L (IN STRAIN B).
SEQUENCE 281 AA; 31845 MW; 241F6AF140995468 CI
                                                                                                                                                                                                          Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horluchi T., "A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map. DNA Res. 3:379-392(1996).
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MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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Submitted (
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SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-Spleen;
STRAINE-98081836; PubMed-9419338;
MEDLINE-98081836; PubMed-9419338;
Hilton D.J., Richardson R.T., Alexander W.S., Viney E.M.,
Hilton D.J., Stari R., Nicholson S.E., Metc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Last Sequence update)
WD repeat and SOCS box containing protein 2 containing WD protein SWiP-2).
WSB2 OR SWIP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WBS2_MOUSE STANDARD;
054929; Q9RIM8;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                  MEDLINE=99284520; PubMed=10354473; Vasillauskas D., Hancock S., Stern C.D.; Vasillauskas D. Devel SOCS box containing WD-protein centres and by Shh during development."; Mech. Dev. 82:79-94(1999).
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EMBL;
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EMBL;
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Electrophoresis 20:2181-2195(1999).
-i- SIMILARITY: STRONG, TO H.INFILUENZAE HI1582/HI1581.
-i- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
FRAMESHIFT IN POSITION 128 THAT PRODUCES TWO SEPARATE ORFS.
      between
                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                              "Twenty proteins classes.";
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Mammalia; Eutheria;
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                        SWISS-PROT entry
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D90830; BBA15692.1; --
L38618; AAA89200.1; ALT_FRAME. L38618; AAA89201.1; ALT_FRAME.
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5; Conserv
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and this statement is not removed.
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ry is copyright. It is produced through a collaboration Institute of Bioinformatics and the EMBL outstation -
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Rodentia;
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SOCS BOX DOMAIN.
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3 -> V (IN REF. 3).
3 -> A (IN REF. 3).
700B8E042FAAA8A5
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Sciurognathi;
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thi; Muridae;
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RESULT 10
DYR2_HUMAN
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Best Local
                                                                                                             specificity of DYRK-related kinases,
specificity protein kinases.";
J. Biol. Chem. 273:25893-25902(1998).
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REPEAT
DOMAIN
CONFLICT
                                                                                                                                                                                                                                                                 Q92630:
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Dual-specificity tyrosine-phosphorylation regulated kinase
(EC 2.7.1.-).
  1 1 1
                                                 Becker W., Joost H.-G.;
Submitted (NOV-1996) to the
-!- FUNCTION: IN VITRO; CAN
                                                                                                                                                       Becker W.,
Joost H.-G.
                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vo
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                TISSUE=Placenta;
                                                                                            SEQUENCE
                                                                                                                                                                          MEDLINE=98421512;
                                                                                                                                                                                             SEQUENCE FROM N.A.
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REPEAT
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SUBCELLULAR LOCATION: Cytoplasmic. PTM: AUTHOPHOSPHORYLATED ON TYR RESIMILARITY: BELONGS TO THE SER/THR
                             AND THR RESIDUES. MAY BE INVOLVED GROWTH AND/OR DEVELOPMENT.
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Pro; IPR001680; WD40.
PF00400; WD40; 6.
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7; Conserv
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Y., Wetzel K., Eirmbter
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PHOSPHORYLATE HISTONES H3 AND
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WD 3.
WD 4.
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(See http://www.isb-sib.ch/announce/
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ERG1_HUMAN STANDARD

Q14534; Q9UEK6;

Q1-NOV-1997 (Rel. 35, C

16-OCT-2001 (Rel. 40, L

16-OCT-2001 (Rel. 40, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prodom: PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1
PROSITE; PS50011; PROTEIN_KINASE_DOM: 1
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
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                     inhibitors in HeLa cells.";
Biol. Chem. 271:8053-8056(1996).
-1- FUNCTION: CATALIZES THE FIRST OXYGENATION :
BIOSYNTHESIS AND IS SUGGESTED TO BE ONE OF ENZYMES IN THIS PATHMAY.
                                                                                                                                                                                                                                                          SEQUENCE OF 187-535 FROM N.A.
                                                                                                                                                                                                                                                                                                        "Localization of the squalene epoxidase chromosome region 8q24.1."; Genomics 44:141-143(1997).
                                                                                                                                                                                                                                                                                                                                                                                      Nagai M., Sakakibara J., Wakui K.,
Tsuji S., Arakawa M., Ono T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=97432831; PubMed=9286711;
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase; Serine/threonine-protein kinase;
ATP-binding; Phosphorylation.
DOMAIN 149 462
DOMAIN 149 462
DOMAIN 155 163
BIND 155 163
BIND 155 163
BINDING 178 178
BINDING 178 178
BINDING 178 178
BINDING 178 178
BY SIMILARITY
ACT_SITE 275 275
BY SIMILARITY
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InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 603496;
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EMBL; Y09216; CAA70418.1; -.
HSSP; Q00534; 1B18.
Genew; HGNC:3093; DYRK2.
                                                                                                                                                    Nakamura Y., Sakakibara J., Izumi T., Shibata A., "Transcriptional regulation of squalene epoxidase
                                                                                                                                                                                                          MEDLINE-96215195;
                                                                                                                                                                                                                                       TISSUE-L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YDODOMVVVQVP 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           528 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141
                                                                                                                                                                                                          PubMed=8626488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59714 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EC
Squalene +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              annotation update)
1.14.99.7) (Squalene epoxidase) (SE)
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF2C6822ED9522D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
AH(2) +
                                                                                                                                                                                                                                                                                                                                                                                                                 Fukushima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ДВ
33;
                                                                                                                                                                                                                                                                                                                                                              gene (SQLE) to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae;
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0(2) -
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                                                STEP
THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 528;
                                                                                                                                                 by s
(S)-squalene-2,3
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RATE-LIMITING
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WARI_ARATH STANDARD; PRT; 168 AA.

WARI_ARATH STANDARD; PRT; 168 AA.

WARIT, 023312;

WARIT_ARATH STANDARD; PRT; 168 AA.

WARIT_1000 (Rel. 33, Created)

WARIT_1000 (Rel. 40, Last sequence update)

WARIT_16-0CT-2001 (Rel. 40, L
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Best Local S
Matches 6
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Genew; HGNC:11279; SQLE.
MIM; 602019; ...
Interpro
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                  STRAIN-CV. Columbia;
MEDLINE-20083488; PubMed-10617198;
Mayer K.F.X., Schueller C., Wambutt R.,
Pohl T., Duesterhoeft A., Stiekema W., F
                                                                                                                                                  MEDLINE-94105161; PubMed-8278386;
Abel S., Oeller P.W., Theologis A.;
"Early auxin-induced genes encode short-lived n
Proc. Natl. Acad. Sci. U.S.A. 91:326-330(1994).
                                                                                                                                                                                                                                                                                                                                       eurosids II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oxidoreductase;
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Pfam; PF01360; Monooxygenase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioliformatics and the EMBL outstation the European Bioliformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
    Harris B.,
                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=3702;
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COFACTOR: FAD.
SUBUNIT: MAY FORM A COMPLEX WITH SQUALENE SYNTHASE.
SUBCELLULAR LOCATION: Microsomal.
SIMILARITY: BELONGS TO THE SQUALENE MONOOXYGENASE FAMILY.
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    Ansorge W.,
                                                                                                                                                                                                                                              Columbia;
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                                                                                                                                                                                                                                                                                                                                  Brassicales;
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                                                                                                             N.A
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    Brandt P.,
                                                                                                                                                                                                                                                                                                                                Brassicaceae;
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FAD (ADP PART) (E
E -> G (IN REF.
R -> Q (IN REF.
L -> P (IN REF.
N -> K (IN REF.
N -> V (IN REF.
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POTENTIAL.
POTENTIAL.
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Pred. No.
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tt R., Murphy G., Volckaert G.,
a W., Entian K.-D., Terryn N.,
Grivell L.A., Rieger M.,
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36;
                                                                                                                                                                                                                                                                                                                                  Arabidopsis
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                                                                                                                                                                           nuclear
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                                                                                                                                                                                                                                                                                                                                                       eudicots;
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RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Pose S., de Haan M., Maarse A.C., Schaefer M., Grimm M., Loehnert T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Piravandi E.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Chark T., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Prishman D., Hasse D., Lencke K., Meyes H.-W., Stocker S.,
RA Prishman D., Hasse D., Lencke K., Meyes H.-W., Stocker S.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Schnoh M., Murray J., Sheet P., Cordes M., Abou-Threideh J.,
RA Schon M., Murray J., Sheet P., Cordes M., Abou-Threideh J.,
RA Fishman D., Fulton B., Miller N., Greco T., Kemp K.,
RA Ramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McComble W.R.;
Thaliana. T., Shong J., Bacthern M., Mactero A., Shah R.,
Sequence and analysis of chromosome 4 of the plant Arabidopsis
                                              Matches
                                                                                                                                                   Multigene family; Nuclear protein; Translation regulation CONFLICT 52 52 A \rightarrow T (IN REF. 1).
                                                                                                                                                                                                               TRANSFAC; T04508;
InterPro; IPR0033
                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Langham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M., Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W., Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
                                                                                                                                                                                                Pfam; PF02309; AUX_IAA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vos P., Hoheisel J., Zimmermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reichert B.,
    2 DQDQMVVVQVPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INDUCTION: BY AUXIN.
SIMILARITY: BELONGS TO THE AUX/IAA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIATING THE VARIOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                          L15448; AAA16569.1; -.
Z97336; CAB10235.1; -.
AL161539; CAB78498.1; -.
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NCTION: COULD ACT AS REGULATOR
                                          Similarity 7; Conser
                                                                                                                                                                                                               IPR003311; AUX_IAA.
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B., Portetelle D., Perez-Alonso M., Boutry
                                                                                                                               168 AA;
                                              Conservative
                                                                                                                               19031 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S REGULATOR OF
AUXIN-INDUCED
                                                                Pred.
                                                                                  Score
                                                                                                                               17CA9B3BEB7962EE
                                          Mismatches
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                                                                No.
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15;
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There are no restrictions
ng as its content is in
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Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Etqu P., Le
Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Etqu P., Le
Toriumi M., Yu G., Brooks S., Chao Q., Chen H., Karlin-Neumann R.
Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P.,
Southwick A., Davis R.W., Ecker J.R., Theologis A.;

"Full length cDNA of gene MXC7-6 (GI:9294192).";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: COULD ACT AS REGULATOR OF GENES RESPONSIBLE FOR
MEDIATING THE VARIOUS AUXIN-INDUCED EVENTS RESPONSIBLE FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clones.";
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                                                                                                              EMBL; L15449; AAA16570.1; -
EMBL; AF027157; AAB97164.1;
EMBL; AB026655; BAB02094.1;
EMBL; AF332392; AAG48756.1;
                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
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Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu "Structural analysis of Arabidopsis thaliana chromo features of the regions of 4,504,864 bp covered by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=cv. Wassilewskija;
Malik M.K., Zimmerman J.L.;
"Molecular characterization of a genomic clone
inducible IAA2 gene from Arabidopsis thaliana."
(In) Plant Gene Register PGR97-178.
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MEDLINE-94105161; PubMed-8278386;
Abel S., Oeller P.W., Theologis A.;
Abariy auxin-induced genes encode short-lived nuclear
Proc. Natl. Acad. Sci. U.S.A. 91:326-330(1994).
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Arabidopsis thaliana (Mouse ear cress).
                                                  TRANSFAC; T04509; -.
InterPro; IPR003311; AUX_IAA.
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  AUX_IAA; 1
ly; Nuclear
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  protein;
Translation regulation
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           AXI4_ARATH
P33077;
01-OCT-1993
01-NOV-1995
15-JUN-2002
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                                                                                                                                                                                                                                     InterPro: IPR03311; AUX_IAA.
Pfam; PF02309; AUX_IAA; 1.
Multigene family; Nuclear protein;
SEQUENCE 179 AA; 20330 MW; 0D21
                                                                                                                                                                                                                                                                                                                                 the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-94016594; PubMed-8411182;

Geller P.W., Keller J.A., Parks J.E., Silbert J.E., Theolog

"Structural characterization of the early indoleacetic acid

genes, PS-TAA4/5 and PS-TAA6, of pea (Pisum sativum L.).";

J. Mol. Biol. 233:789-798(1993).

-i- FUNCTION: COULD ACT AS REGULATOR OF GENES RESPONSIBLE FOR THE VARIOUS AUXIN-INDUCED EVENTS RESPONSIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pisum sativum (Garden pea).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
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Auxin-responsive protein IAA4 (Indoleacetic
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7; Conservative
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174 AA;
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(Rel. 32, Last seq
(Rel. 41, Last ann
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19910 MW;
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58.3%;
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; Pred. No. 16;
1; Mismatches
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DECA4F59F0106179 CRC64;
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tic acid-inducible
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Query Match
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STRAIN-CV. Columbia;

Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Etgu P., Le

Toriumi M., Yu G., Brooks S., Chao Q., Chen H., Karlin-Neumann

Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P.,

Southwick A., Davis R.W., Ecker J.R., Theologis A.;

"Full length cDNA of gene MQD19.3 (GI:10177938).";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: COULD ACT AS REGULATOR OF GENES RESPONSIBLE FOR

MEDIATING THE VARIOUS AUXIN-INDUCED EVENTS RESPONSIBLE FOR
                                                                                                                                                                     TRÂNSFAC; T04511;
InterPro; IPR003311; AUX_IAA.
Pfam; PF02309; AUX_IAA; 1.
Multigene family; Nuclear protein;
Multigene family; Nuclear protein;
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MEDLINE=91338700; PubMed=2102379;
Conner T.W., Goekjian V.H., Lafayette P.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Auxin-induced protein AUX2-11).
IAA4 OR AUX2-11 OR ATSC43700 OR MQD19.3.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosic
                                                                                                                                                                                                                                                                                                    EMBL;
PIR; (
                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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TRANSFAC; T04511; -.
InterPro; IPR003311;
                                                                                                                                                                                                                                                                                                                     EMBL; X53435; CAA37526.1; -. EMBL; L15450; AAA16571.1; -. EMBL; AB026651; BAB11297.1; -. EMBL; AF332394; AAG48758.1; -.
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Kaneko T., Katoh T.,
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MEDLINE=94105161; PubMed=8278386;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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149
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SIMILARITY: BELONGS TO THE AUX/IAA FAMILY.
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Search completed: March 27, 2003, 10:04:18 Job time : 3.30488 secs

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Q23SH1
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Q9LYN1
Q9LYN1
Q9LYN1
Q9BJ1
Q9BJ1
Q8BJ3
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Q9EBN7
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O9lqe3 arabidopsis
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O9832 arabidopsis
O9c3311 arabidopsis
O9xid4 arabidopsis
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O9l118 rhizobium 1
O8ujb3 agrobacteri
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O8ujb3 onteromorph
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O39281 equine herp
O9c8n7 arabidopsis
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0 enteromorph
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1 equine herp
7 arabidopsis
8 arabidopsis
5 pisum sativ
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ALIGNMENTS

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Best Local Similarity
Matches 14; Conserv
   Q9FND9;
Q9FND9;
01-MAR-2001
01-MAR-2001
01-JUN-2002
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09ZT62;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-LEAF;
Ohsumi C., Nozaki J., Kida T.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF073744; AAD02832.1; -.
Glycosyltransferase; Transferase.
SEQUENCE 784 AA; 86920 MW; 3B06A491F0908933 CRC64;
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Q9LQE3;
01-OCT-2000
                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core «
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen E. Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozak Ecker J., Theologis A., Davis R.W., Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AM06702; BAB11595.1; -. EMBL, AV081645; AAM10207.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome 5. Sequence features of the regions of 1,044,062 bp covered b physically assigned Pl clones.";
DNA Res. 4:291-300(1997).
  Cheuk R., Shinn
                                       Submitted
                                                                                         Submitted
                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                    01-OCT-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                Ecker J
                                                               SEQUENCE FROM
                                                                                                                                          NCBI_TaxID=3702;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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MEDLINE=98069011; PubMed=9405937;
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Pred. No. 2.6;
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Submitted (JUN-2000) to the EMBL/GenBank/EEMBL; AC007887; AAF79360.1; -.
InterPro: IPR003340; TF_B3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q38832 PRELIMINARY;
Q38832;
01-NOV-1996 (TrEMBLrel. 01-NOV-1996 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel. 1
                                                                                            Q9C5W8;
Q9C5W8;
01-JUN-2001
01-JUN-2001
01-DEC-2001
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Lee J., Lenz C., Li J
Nguyen M., Palm C., F
Thaveri A., Toriumi N
                             Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                          Pfam; PI
NON_TER
                                                                        D13315C/AT4G14550
                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress). Embry, Eukaryota; Viridiplantae; Streptophyta; Embry, Spermatophyta; Magnoliophyta; eudicotyledons; eurosids II; Brassicales; Brassicaceae; Arabi(NCBI_TaxID=3702;
 SEQUENCE
                 NCBI_TaxID=3702;
                                                                                    IAA14
                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                           EMBL;
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                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=95387393; PubMed=7658471;
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                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
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ENCE 570
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U18416; AAC49055.1; -.
                                                                                                                                                                                                                                                                                                   PF02309; AUX_IAA; 1.
                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                164 AA;
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9.9;
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Schwartz J., Southwick A.
G., Davis R., Federspiel
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Howing B.,
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C Q9XID4;
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T 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 21, Last sequence upc
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation of the feather of the fe
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Best Local
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Best Local :
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023311;
01-JAN-1998
01-NOV-1999
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last senotation update)
IAA7-like protein (IAA7 like protein).
DL3315C OR AT4G14550.
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF334718; AAG55096.1; -.
InterPro; IPR003311; AUX_IAA.
Pfam; PF02309; AUX_IAA; 1.
SEQUENCE 228 AA; 25044 MW; A76A9F733538E372 CRC64;
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Goldsmith A.D., Lee J.M., Toriumi M., Yu G., Bar
Chen H., Karlin Neumann G., Kim C., Lam B., Miz
Palm C.J., Shinn P., Southwick A., Davis R.W.,
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Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Submitted (MAR-2000) to the EM
EMBL: 297336; CAB46059.1;
EMBL: AL161539; CAB78497.1;
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NCE 234 AA; 256
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8; Conserv
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Thim1 M., Yu G., Brooks S.
Broker
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ne EMBL/GenBank/DDBJ
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Pred. No.
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5.7;
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s S., Chao
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RESULT
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              Query Match
                                                                               InterPro: IPR001611; LRR.
InterPro: IPR003592; LRR_out.
Pfam; PF00560; LRR; 7.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00019; LEURICHRPT.
PRODOM; PD000001; Euk_pkinase; 1.
SMART; SM00370; LRR; 6.
                                                                                                                                                                                                                                                                                                                                                                                                        Q9LYN1;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 77.3 kDa protein.
F18021_60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AC007454; AAD39615.1; -.
InterPro; IPR003311; AUX_IAA.
InterPro; IPR003340; TF_B3.
Pfam; PF02309; AUX_IAA; 1.
Pfam; PF02362; B3; 1.
SEQUENCE 619 AA; 69995 MW; 1DA4DD7BC43927E7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                       PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Hypothetical protein; Transferase
SEQUENCE 719 AA; 77329 MW; 3B91891A64E0DFD
                                                                                                                                                                              EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL163763; CAB87409.1; -
InterPro; IPR000719; Euk_Pkinase.
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Lemcke K., Mayer K.F.X.,
Submitted (APR-2000) to 1
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
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STRAIN=CV. COLUMBIA;
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STRAIN=CV. COLUMBIA;
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7; Conserv
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53.8%;
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o the EMBL/GenBank/DDBJ databases.
  Score 44;
Pred. No.
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Pred. No. 16;
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                                           3B91891A64E0DFD3 CRC64;
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Matches 6
SEQUENCE FROM N.A.

MEDLINE-21608550; PubMed-11743193;

MEDLINE-21608550; PubMed-11743193;

MOOD D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

Zhang S., Yoo H., Tao Y., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8UJB3;
                                                                                                                                                                                                                                                                                                                                                                                   Agrobacterium tumefaciens (strain C58 / ATCC Bacteria; Proteobacteria; alpha subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                  DEPA OR ATUO015 OR AGR_C_24 Agrobacterium tumefaciens (s
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InterPro; IPR002104; Phage_integrase; 1.
Pfam; PF00589; Phage_integrase; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Plasmid; Complete proteome.
SEQUENCE 416 AA; 46416 MW; 1DAB19
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01-OCT-2001
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DNA Res. 7:331-338(2000).
EMBL; AP003015; BAB54691.1; -.
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01-JUN-2002 (TrEMBLrel.
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21, Last annotation update)
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Rhizobiaceae
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RESULT 12 Q8S3B5 ID Q8S3B AC Q8S3B

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"Genome sequence of the plant pa
Agrobacterium tumefaciens C58.";
Science 294:2323-2328(2001).
EMBL; AE008976; AAL41046.1; -.
EMBL; AE007944; AAK85840.1; -.
                                                                                                                                                                                                                                                                                                                                                       O81350 PRELIMINAMI,
O81350;
O81350;
O1-NOV-1998 (TrEMBLrel. 08, Created)
O1-NOV-1998 (TrEMBLrel. 08, Last sequence update)
O1-NOV-1998 (TrEMBLrel. 21, Last annotation updat
5'-adenyly.sulfate reductase (EC 1.8.99).
5'-adenyly.sulfate reductase (EC 1.8.99).
5'-adenyly.sulfate reductase (EC 1.8.99).
                                                                                                                                                                                    macroalga Enteromorpha intestinalis.";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases

EMBL; AF069951; AAC26855.1; -

InterPro; IPR004508; APS_reduc.

InterPro; IPR002500; PAPS_reduct.

InterPro; IPR002500; Thiored.
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Gao Y., Leustek T.;

Gao In Gardenylylsulfate (APS) reductase from the "Cloning of 5'-adenylylsulfate (APS) reductase from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz Wollam C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science [2]
                                                                                                       Oxidoreductase.
SEQUENCE 423 AA;
                                                                                                                                               Pfam; PF01507; PAPS_reduct; 1. Pfam; PF00085; thiored; 1. PRINTS; PR00421; THIOREDOXIN.
                                                                                                                                                                                                                                                                                                                            Enteromorpha.
NCBI_TaxID=3116;
                                                                                                                                                                                                                                                                                                                                                       Enteromorpha intestinalis (Hollow green seaweed).
Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Ulvales; Ulvaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome.
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MEDLINE=21608551; PubMed=11743194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The genome C58.";
                                                                                                                                   TIGRFAMS; TIGR00424;
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330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242
                         2 DQDQMVVVQVPW 13
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DKDTMVVLYAPW
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                                                    Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              418 AA;
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the natural genetic
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341
                                                                                                        46808
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                                                                 58.3%;
                                                                                                                                 APS_reduc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.8%;
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                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                 Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pathogen and biotechnology agent ^{\rm n};
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J.-F., Gordon M.P.,
                                                                                                        808EE4F3BD56F1F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6664887C7A732B34 CRC64;
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17;
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. 16;
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                                                                             Length 423;
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                                                     Indels
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039281;
01-JAN-1998
01-JAN-1998
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CV. KINGSTON:
Shan X., Martin R.C., Mok D.
Submitted (MAR-2002) to the
EMBL; AF489877; AAM09517.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Putative glucosyltransferase.

Phaseolus lunatus (Lina bean) (Phaseolus limensis).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;

eurosids I, Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
                                                                             Telford E.A., Watson M.S., Perry Submitted (OCT-1997) to the EMBL/. EMBL, AF030027; AAC59558.1; -. InterPro: IPR004936; Herpes_UL21. Pfam; PF03252; UL21; 1. SEQUENCE 529 AA; 58150 MW; E2
                                                                                                                                                           MEDLINE-98264497; PubMed-9603335;
Telford E.A., Watson M.S., Perry J., Cullina:
"The DNA sequence of equinc herpesvirus-4.";
J. Gen. Virol. 79:1197-1203(1998).
                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                           "The
                                                                                                                                                                                                                                                    Nicolson L.,
                                                                                                                                                                                                                                                                       STRAIN-NS80567;
                                                                                                                                                                                                                                                                                                        Viruses; dsDNA viruses, no RNA stage;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                         Equine herpesvirus 4.
                                                                                                                                                                                                                                                                                                                                           Counterpart
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3884;
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                 STRAIN-NS80567;
                                                                                                                                                                                               STRAIN-NS80567
                                                                                                                                                                                                          SEQUENCE FROM
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                                                                                                                                                                                                                                                                              SEQUENCE OF 489-529 FROM N.A.
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        283
                                                                                                                                            EQUENCE FROM
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                                                                                                                                                                                                                                 olson L., Cullinane A.A., Onions D.E e nucleotide sequence of an equine he herpes simplex virus 1 glycoprotein
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                          DOMVVVQVPWP 14
        DEIILVEEPWP 293
                                           Similarity
5; Conserv
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7; Conser
                                                                                                                                                                                                                         Virol.
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(TremBLrel. 05, Last sequence update)
(TremBLrel. 21, Last annotation update)
of HSV-1 gene UL21 and VZV gene 38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                           N.A.
                                                                                                                                                                                                        N.A.
                                                                                                                                                                                                                          71:1793-1800(1990).
                                                                                                                                                                                                                                                            PubMed-2167933;
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                                                    52.5%;
45.5%;
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53.8%;
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                                            5.
                                                                                                                EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42;
Pred. No.
                                        Pred. No. 32;
5; Mismatches
                                                    Score 42;
Pred. No.
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                                                                             E2B737B89D489413 CRC64;
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Bank/DDBJ databases
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28;
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Q9LQE8
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01-JUN-2001
01-JUN-2002
                                                                                                      Q9LQE8;
01-OCT-2000
01-OCT-2000
01-JUN-2002
                Ecker J.R.
Submitted
                        SEQUENCE
Ecker J.R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9C8N7;
                                                                                                                                         09LQE8
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                                                  NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                         thaliana.
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RC STRAIN-CV. COLUMBIA;

RM MEDLINE-20105719; PubMed-11130712;

RA MEDLINE-21016719; PubMed-11130712;

RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA Theologis A., Ecker J.R., Palm C.J., Ecker S.Y.,

Branch C.J., Alonso J., Altaii H., Araujo R., Bowman C.L., Brooks S.Y.,

RA White O., Alonso J., Altaii H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Chao Q., Chen H., Feng J.-D., Fong B., Fujii C.Y.,

RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Langin-Hooper S., Lee A., Luros J.S., Maitt R., Marziali A.,

RA Langin-Hooper S., Liu S.A., Luros J.S., Maitt R., Marziali A.,

RA Langin-Hopper S., Liu S.A., Luros J.S., Maitt R., Marziali A.,

RA Hillscher J., Miranda M., Nujuyen M., Nijerman W.C., Osborne B.I.,

RA Langin-Hopper S., Liu S.A., Luros J.S., Maitt R., Marziali A.,

RA Militscher J., Miranda M., Nujuyen M., Nooney T., Rowley D.,

RA Alin X., Liu S.X., Liu Z.A., Luros J.S., Maitt R., Marziali A.,

RA Militscher J., Miranda M., Nujuyen M., Rooney T., Rowley D.,

RA Sakano H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Sakano H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Witchenback T., Van Aken S., Vaysberg M., Poroney T.,

RA Witchenback T., Van Aken S., Vaysber
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Auxin response factor, putative. F7P12.6.
                                                                                                                                                                                                                             Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embry.
Spermatophyta; Magnollophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003311; AUX_IAA.
InterPro; IPR003340; TF_B3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 408:816-820(2000).
EMBL; AC023913; AAG51894.1;
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PF02362; B3; 1.
NCE 600 AA; 67933 MW;
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(TrEMBLrel. 17, Last
(TrEMBLrel. 21, Last
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                                                               EMBL/GenBank/DDBJ databases
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Pred. No.
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                                                                                                                                                                                                                                                                 core eudicots; Rosidae;
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RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

RI Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,

RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,

RA Cheuk R., Schinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,

RA Cheuk R., Schinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,

RA Cheuk R., Schinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,

RA Cheuk R., Schinn P., Brooks S., Echer J.,

RA Cheuk R., Schinn P., Brooks S., Hansen N., Howing B., Koo T., Lam B.,

RA Cheuk R., Schinn P., Sakano H., Schwartz J., Southwick A.,

RA Theologis A., Ecker J.;

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Result
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

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10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

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Match
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US-09-754-853A-1111
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Sequence 14, Appl Sequence 1105, Ap Sequence 1105, Ap Sequence 1111, Ap Sequence 1111, Ap Sequence 1112, Ap Sequence 11102, Ap Sequence 11104, Ap Sequence 11104, Ap Sequence 11114, Ap Sequence 11114, Ap Sequence 11119, Ap Sequence 11017, Appl Sequence 11017, Ap Sequence 11017, A
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Sequence 3614, Ap	Sequence 2, Appli	Sequence 1320, Ap	Sequence 4, Appli	Sequence 10944, A	Sequence 265, App	Sequence 66, Appl		Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appl1	6	Sequence 2, Appli	Sequence 29, Appl	Sequence 10, Appl	Sequence 2, Appli		Sequence 1, Appli	Sequence 50, Appl	Sequence 5, Appli	Sequence 1107, Ap	Sequence 1107, Ap	Sequence 2, Appli	Sequence 21, Appl	Sequence 1108, Ap	Sequence 1106, Ap

ALIGNMENTS

RESULT 1 US-09-772-134B-14

Sequence 14,

Application US/09772134B

GENERAL INFORMATION:

Patent No. US20020144310A1

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RESULT 2
US-09-754-853A-1103
; Sequence 1103, Application US/09754853A
; Publication No. US20030005491A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      ; ORGANISM: soybean ; FEATURE; NAME/KEY: misc_feature ; LOCATION: (1)..(830) ; OTHER INFORMATION: Xaa is any amino acid US-09-772-134B-14
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SEQ ID NO 14
LENCTH: 830
TYPE: PRT
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Best Local Similarity
Matches 6; Conserv
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APPLICANT: Lightfoot, David
APPLICANT: Lightfoot, David
APPLICANT: Lightfoot, David
APPLICANT: Meksem, Khalid
TITLE OF INVENTION: ISOLATED POLYNUCLEOTIDES AND POLYPEPTIDES RELATING TO LOCI UND
TITLE OF INVENTION: RESISTANCE TO SOYBEAN CYST NEMATODE AND SOYBEAN SUDDEN DEATH
TITLE OF INVENTION: METHODS EMPLOYING SAME
FILLE REFERENCE: 1268/4/2
CURRENT APPLICATION NUMBER: US/09/772,134B
CURRENT APPLICATION NUMBER: US/09/772,134B
CURRENT FILING DATE: 2001-01-28
PRIOR APPLICATION DATE: 2001-01-28
NUMBER OF SEQ ID NOS: 122
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54.5%;
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Pred. No.
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; OTHER INFORMATION: Clone ID: rhgl_peking_amplicon
US-09-754-853A-1103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 1105
LENGTH: 854
TYPE: PRT
                                                                                                  GENERAL INFORMATION:
                                                                                                                Sequence 1111, Application US/09754853A Publication No. US20030005491A1
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APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
                                  APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
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APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
                    APPLICANT:
TITLE
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OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
                    Wang, Ming Li
                                                                                                                                                                                                                                                                                                                    Conservative
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APPLICANT: Hauge, Brian M.

APPLICANT: Parnell, Laurence D.

APPLICANT: Parsons, Jeremy D.

APPLICANT: Wang, Ming Li

TITLE OF INVENTION: Nucleic Acid Molecules An
TITLE OF INVENTION: Soybean Cyst Nematode Re
FILE REFERENCE: 38-10(15810)8

CURRENT APPLICATION NUMBER: US/09/754,853A

CURRENT FILING DATE: 2001-01-05
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                                                                                                                                                                                                                                                                                                                                                       Sequence 1115, Application US/09754853A Publication No. US20030005491A1 GENERAL INFORMATION:
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SEQ ID NO 1113
LENGTH: 854
TYPE: PRT
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SEQ ID NO 1111
LENGTH: 854
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Best Local :
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APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10 (15810)8
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PRIOR FILING DATE: 2000-01-07
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                                                                                                                             Resistance
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PRIOR APPLICATION NUMBER:

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APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REPERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR EPILICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
SEO ID NO 1102
LENGTH: 877
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
COTHER TO
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Arplicant: Wang, Ming Li
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 1104
LENGTH: 877
TYPE: DPT
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NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 1115
LENGTH: 854
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Best Local :
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nes 6; Conserv
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54.5%;
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Pred. No. 10;
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APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And
TITLE OF INVENTION: Soybean Cyst Nematode Re:
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEO ID NOS: 1119
SEO ID NO 1112
LENGTH: 877
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; OTHER INFORMATION: Clone ID: rhg1_lee_amplicon US-09-754-853a-1112
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US-09-754-853A-1112
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                                                                                                                                                                                                                                                                                                                APPLICANT: Hauge, E
APPLICANT: Parnell
APPLICANT: Parsons
APPLICANT: Wang, M
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                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1112, Application US/09754853A Publication No. US20030005491A1
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Best Local :
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APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
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APPLICANT: Parnell, Laurer
APPLICANT: Parsons, Jerem
APPLICANT: Wang, Ming Li
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TYPE: PRT
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                                     ORGANISM: Glycine max FEATURE:
                                                                              TYPE: PRT
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Local Similarity 54.5%;
es 6; Conservation
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 11;
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US-09-754-853A-1114
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PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 1114
LENGTH: 877
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Acomica-X-1
                                                                                                                                                                                 PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Clone ID: rhg1_pi200499_amplicon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 QGQVIVIQLPW 148
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nes 6; Conserv
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                                                                                                                    APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
                                                                                                                                                        FILING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
                                                                            APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664 FILING DATE: 2001-01-30
                                      FILING DATE:
                                                         APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
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Pred. No.
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Pred. No.
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ORGANISM:
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CURRENT FILING DATE: 2001-03-06

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09-09-09

PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-09

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60-03-12

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60-03-12

PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12

PRIOR PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60-03-12

PRIOR PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60-03-12

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60-03-12
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SOFTWARE: Pa
SEQ ID NO 50
LENGTH: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 50, Application US/09798889 Publication No. US20030004324A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: 31 Human secreted proteins
FILE REFERENCE: PZ026P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: I OTHER INFORMATION: I OTHER INFORMATION: I OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/798,889
CURRENT FILING DATE: 2001-03-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/234,687 PRIOR FILING DATE: 2000-09-21 PRIOR APPLICATION NUMBER: US 09/608,408 PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR PRIOR
                                                                         NUMBER OF SEQ ID NOS: 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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                                                    Patentin
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EXPRESSED IN BRAIN, SIGNAL = 1.5
EXPRESSED IN ADULT LIVER, SIGNAL = 3.5
EXPRESSED IN LUNG, SIGNAL = 2.2
EXPRESSED IN BONE MARROW, SIGNAL = 1.2
EXPRESSED IN PLACENTA, SIGNAL = 1.4
EXPRESSED IN HELA, SIGNAL = 1.7
EXT_HUMAN HIT: AM962016.1, EVALUE 2.00e-23
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Pred. No.
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                                                                                                                             60/077,696
                                                                                                                                                                                                                                60/077,686
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Homo

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APPLICANT: Parsons, Jeremy D.

APPLICANT: Wang, Ming Li

TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With

TITLE OF INVENTION: Number: US/09/754,853A

CURRENT APPLICATION NUMBER: US/09/754,853A

CURRENT APPLICATION NUMBER: US/09/754,853A

CURRENT FILING DATE: 2001-01-05

PRIOR APPLICATION NUMBER: US 60/174,880

PRIOR FILING DATE: 2000-01-07

NUMBER OF SEQ ID NOS: 1119

SEQ ID NO 1101

LENGTH: 854

TYPE: PRT

ORGANTT
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; NAME/KEY: SITE
; LOCATION: (46)
; OTHER INFORMATION: Xaa equals stop translation
US-09-798-889-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
THER INFORMATION: Clone ID: 240017_region_G3
US-09-754-853A-1098
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; OTHER INFORMATION: Clone ID: rhgl_A3244_amplicon US-09-754-853A-1101
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Best Local Similarity bo.,
Conservative
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Best Local Similarity 55.0
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 1098
LENGTH: 854
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1098, Application US/09754853A Publication No. US20030005491A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
                                ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1::|:|:|
117 QVIVIQLPW 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :||| :|||
18 LVVVSLPWP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 QMVVVQVPW 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 9; Length 854; Pred. No. 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Query Match

50.0%; Score 40; DB 9; Length 854;

Best Local Similarity 55.6%; Pred. No. 52;

Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps

Qy 5 QMVVVQVPW 13

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Db 117 QVIVIQLPW 125
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Search completed: March 27, 2003, 10:20:37 Job time: 4.2439 secs

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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     of hits satisfying chosen parameters:
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length: 2000000000
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1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/laa/backfiles1.pep:*
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Match Length
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Gapop 10.0 , Gapext 0.5
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     PVSVGCFVGFDASEPDSRH
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US-08-846-234-2
US-08-955-223-450
US-08-955-223-4460
US-08-861-774E-22
US-08-861-774E-34
US-09-105-697-5
US-09-105-697-6
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US-09-105-697-6
US-08-24-359A-6
US-08-384-490-31
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PVSVGCFVGFDASEPDSRH	ilarity Conserva	CATION NOME CATION 1 : (703)-4 (703)-4 OR SEQ 1 ARACTER1 19 aming ino acid linear PE: per PE: int	ZIP: 22202 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compati OPERATING SYSTEM: PC-DOS SOFTWARE: Patentin Relea CURERNT APPLICATION DATA: APPLICATION NUMBER: US/O FILING DATE: APPLICATION NUMBER: US/O FILING DATE: NORMAN F. OBLON NAME: NORMAN F. OBLON	IDENCE ADDRESS: IEE: OBLON, SE 1755 S. JEFF ARLINGTON VIRGINIA	uence 2, Application Uent No. 6166292 ent No. 6166292 NERAL INFORMATION: APPLICANT: NOZAKI Jin APPLICANT: KIDA TAKAO TITLE OF INVENTION: R TITLE OF INVENTION: R NIMBER OF SECULENCES.	• •		38.1 38.1 38.1 38.1 37.6
EPDSRH EPDSRH	100 100 tive	INFORMA (NFORMA) (1413-33-13-222 ID NO: ISTICS: O acids of tide Cernal	FORM: FORM: Floppy disk Floppy disk Compatible FORM: FC-DOS/MS FATENTION DATA: NUMBER: US/08/8 T INFORMATION: T INFORMATION:	E S	US iek ins ao ao RA PR		560 560 597 833 833	88888888888888888888888888888888888888
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	ore 105; ed. No. 2e Mismatches			MCCLELLAND, DAVIS HIGHW	4 SYNTHASE RAFFINOSE	ALIGNMENTS	US95-1 US95-1 US95-1 US95-1 US95-1 08-073- 8-254- 8-483-	3591-0 3591-0 3591-0 3595-1 3595-1 3595-1 3595-1
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Best Local Similarity
Matches 19; Conserv
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Patent No. 6166292
GENERAL INFORMATION:
APPLICANT: NOZUMI Chieko
APPLICANT: NOZAKI Jinshi
APPLICANT: KIDA Takao
                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                         APPLICANT: Edwarus,
APPLICANT: Duelert, Aymeric
APPLICANT: Lacroix, Bruno
APPLICANT: Lacroix, Bruno
TANVENTION: 5' ESTS FOR SECRETED PROTEINS
                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
                                                                                                                                                                                                NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 784 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                SOFTWARE: Word CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: RAFFINOSE SYNTHASE GENE, METHOD FOR TITLE OF INVENTION: PRODUCING RAFFINOSE, AND TRANSGENIC PLANT NUMBER OF SEQUENCES: 22
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                                                                                                                                                        STREET: 501 West I
CITY: San Diego
STATE: California
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APPLICATION NUMBER:
                                                                                                                            ZIP: 92101-3505
                                                                                                                                           COUNTRY:
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ZIP: 22202
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(703)-413-2220
TD NO: 5:
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Pred. No. 1.2e-08;
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                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/08/861,774E
CURRENT FILING DATE: 1997-05-22
NUMBER OF SEO ID NOS: 94
SOFTWARE: Patentin ver. 2.0
SEO ID NO 22
LENGTH: 212
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Waters, Barbara
APPLICANT: Miao, Vivian
APPLICANT: Ho, Yap
APPLICANT: Tong, Seow
                                                         Best Local Similarity Matches 7; Conserv
                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 36. Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR TITLE OF INVENTION: BIOACTIVE MOLECULES FILE REFERENCE: 9993-006
                                                                                                                              NAME/KEY: SITE
LOCATION: (136)
OTHER INFORMATION: Xaa=unknown amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (619) 235-01
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                            ORGANISM: Xanthoparmelia cumberlandia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: PROTEIN ORIGINAL SOURCE: ORGANISM: Homo Sapiens
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LENGTH: 22 amino acids
TYPE: AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
22
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IDENTIFICATION METHOD:
OTHER INFORMATION: seq
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                            1 PVSVGCFVGFDASEPD 16
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PEDVGCYIGACATDYD 37
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Tong, Se
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                                                           Conservative
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36.8%;
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Pred. No. 2
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RESULT 5 US-08-861-774E-34 ; Sequence 34, Application US/08861774E

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APPLICANT: Tong, Seow
TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR
TITLE OF INVENTION: BIOACTIVE MOLECULES
FILE REFERENCE: 993-006
CURRENT APPLICATION NUMBER: US/08/861,774E
CURRENT FILING DATE: 1997-05-22
NUMBER OF SEO ID NOS: 94
SOFTWARE: Patentin Ver. 2.0
SEO ID NO 34
LENGTH: 212
TYPE: PRT
ORGANISM: Leptogium corniculatum
US-08-861-774E-34
Query Match
Best Local Similarity f
"""ches 8; Conservat
                                                                                         ; MOLECULE TYPE: US-09-105-697-4
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Best Local Similarity 43.8%;
Matches 7; Conservative
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APPLICANT:
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APPLICANT: Miao, Vivian
APPLICANT: Ho, Yap
                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Petry Ph.D., Douglas A.
REGISTRATION NUMBER: 35321
REFERENCE/DOCKET NUMBER: 1043
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510)814-2974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                 TELEFAX: (510)814-2977
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gelfand Ph.D., David H.
APPLICANT: Reichert, Fred L.
TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Branchburg
STATE: New Jersey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 PEDVGCYIGACATDYD 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/105,697
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1080 U.S. Highway 202
                  Conservative
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                                                                                                         protein
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                                     38.1%;
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                                     Score 40; DB Pred. No. 75;
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US-09-105-697-5
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                                                                                                                                                                                                                                                      Sequence 6, Applica
Patent No. 6228628
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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ZIP: 08876

ZIP: 08876

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS

COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Gelfand Ph.D.,
APPLICANT: Reichert, Fred
APPLICANT: Reichert, Fred
                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (510)814-2977 INFORMATION FOR SEQ ID NO:
                                                                                                                                                             APPLICANT: Gelfand Ph.D., David H.
APPLICANT: Reichert, Fred L.
TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Petry Ph.D., Douglas A.
REGISTRATION NUMBER: 35321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                     STREET: 1080 U.S. CITY: Branchburg STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                             38.1%;
Local Similarity 61.5%;
les 8; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1080 U.S. CITY: Branchburg STATE: New Jersey
                                         COUNTRY: U
ZIP: 08876
                                                                                                                                                                                                                                                                                                                                                                   64 FVVFDAKAPSFRH 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
TOPOLOGY: lir
                                                                                                       ADDRESSEE: Roche Molecular Systems
STREET: 1080 U.S. Highway 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/105,697 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                   7 FVGFDASEPDSRH 19
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1080 U.S. Highway 202
                                                      United States
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Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB
Pred. No. 75;
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RESULT 9
US-07-977-434-8
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Best Local :
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                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 590
FILING DATE: 28-SEP-1990
PRIOR APPLICATION UNMBER: US 590
APPLICATION NUMBER: US 590
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                 COMPUTER: Macintosh
OPERATING SYSTEM: 7
SOFTWARE: WORDERFICK 2.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07,
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5 TO 3' EXONUCLEASE MUTATIONS
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (510)814-2974
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NAME: Petry Ph.D., Douglas A.
REGISTRATION NUMBER: 35321
                                                                                                           PRIOR APPLICATION DATA:
                                                   PRIOR APPLICATION DATA:
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                                                                       APPLICATION NUMBER: US 523,394 FILING DATE: 15-MAY-1990
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Local Similarity 61.5%;
les 8; Conserva+4...
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                             APPLICATION NUMBER: US 5 FILING DATE: 28-SEP-1990
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New Jersey ZIP: 07110-1199
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12-JAN-1988
)N DATA:
                                    US 143,441
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Pred. No.
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RESULT 10
US-07-977-434-10
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APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (510) 814-2972 INFORMATION FOR SEQ ID NO: 8:
                                                                                  COMPUTER: Macintosh OPERATING SYSTEM: 7
SOFTWARE: WordPerfect 2.1
CURRENT APPLICATION DATA:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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ATTORNEY/AGENT INFORMATION:
NAME: Luann Cserr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER:
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FILING DATE: 17-JUN-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                     ADDRESSEE:
STREET: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.18;
Local Similarity 61.58;
nes 8; Conservativo
                                                                                                                                                                                      STATE: New Jersey
ZIP: 07110-1199
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                                                  APPLICATION NUMBER: US/07/977,434 FILING DATE:
                                                                                                                                                                                                                          CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 FVVFDAKAPSFRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid TOPOLOGY: linear
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REFERENCE/DOCKET NUMBER: Case No. 5466591 8753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 FVGFDASEPDSRH 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  834 amino acids
                                                                                                                                                                                                                                     E: Hoffmann-La Roche Inc.
340 Kingsland Street
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24-JUL-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76
                                                                                                                                                                                                                                                                                                         THERMOSTABLE
                                                                                                                                                                                                                                                                                                                         5' TO 3' EXONUCLEASE MUTATIONS
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   US 590,490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US 455,611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 1; Pred, No. 2.4e+02; Indels
                                                                                                                                                                                                                                                                                                           DNA POLYMERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 834;
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APPLICATION NUMBER: US 5 FILING DATE: 28-SEP-1990

28-SEP-1990

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                                                                                                                                   Sequence 6, Application US/08073384C Patent No. 5541311 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
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ATTORNEY/AGENT INFORMATION:
NAME: LUGBN CSETT
REGISTBAMTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 12-um.
FILING DATE: 12-um.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US OF
APPLICATION NUMBER: 17-UN-1987
                              TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                               APPLICANT: Dahlberg, James E. APPLICANT: Lyamichev, Victor I. APPLICANT: Brow, Mary Ann D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 17 FILING DATE: 02-NOV-PRIOR APPLICATION DATA:
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FILING DATE: 15-MAY-
PRIOR APPLICATION DATA:
                 CORRESPONDENCE ADDRESS
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: Case No. 5466591 8753
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FILING DATE: 22-AUG-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                        7 FVGFDASEPDSRH 19
                                                                                                                                                                                                                                                                                                                              Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                              Conservative
HAVERSTOCK, MEDLEN & CARROLL
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20-SEP-1990
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                                                                                                                                                                                                                                                                                                                                              38.1%;
                                   POLYMERASE
29
                                                                  SYNTHESIS-DEFICIENT THERMOSTABLE DNA
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Pred. No. 2.4e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                            .4e+02;
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                                                                                                                                                                                                                                                                                                                                                             Length 834;
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US-08-254-359A-6
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08254359A Patent No. 5614402
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DAHLBERG, JAMES E.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: BROW, MARY ANN D.
TITLE OF INVENTION: 5' NUCLEASES DERI
TITLE OF INVENTION: DNA POLYMERASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:
MEDITEN & CAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415/397-8338 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CASTOIL DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPETWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,359A
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MEDIUM TYPE: Floppy disk
COMPUTER: IDM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COETHANDE: Patostin Pc-Dos/MS-DOS
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                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 06-JUN-1993
                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: Unit-
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CITY: San Francisco
                                                                                                                                                                                                                                                                                                          ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
                                                                           FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 FVVFDAKAPSFRH 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Carroll, Peter G. REGISTRATION NUMBER: 32,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/01 FILING DATE: 04-JUN-1993
                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                         94104
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Similarity 61.5%;
8; Conservative
                                                                                                                                                                                                                                                                                             CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                           LYAMICHEV, VICTUR 1.
BROW, MARY ANN D.
BROW, MARY ANN D.
WENTION: 5' NUCLEASES DERIVED FROM THERMOSTABLE
                                                                                                                                                                                                                                                                         UNITED STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                           OF AMERICA
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Pred. No. 2.4e+02;
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FILING DATE: APPLICATION NUMBER:

07-DEC-1992

US 07/986,330

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RESULT 13
US-08-384-490-31
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US-08-384-490-31
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                                                                              TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acids
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acids
               MOLECULE TYPE:
                                                                                                                                               REFERENCE/DOCKET NUMBER: 88
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2863
                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Slas, Stacey R.
REGISTRATION NUMBER: 32,630
                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,490
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gelfand, David H.
APPLICANT: Lawyer, Frances C.
APPLICANT: Stoffel, Susanne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY:
STATE:
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Local Similarity 61.5%;
nes 8; Conservativo
                             STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: single
                                                                  TYPE:
                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 FVGFDASEPDSRH 19
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                                                                amino acid
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: U.S.A.
                                                                             834 amino acids
                                 linear
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               DNA (genomic)
                                             single
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Pred. No. 2.4e+02;
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US-08-459-383-31

) Sequence 31, Application US/08459383

) Patent No. 5741690

) GENERAL INFORMATION:
                                                                         RESULT 15
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US-08-483-043-6
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Best Local Similarity
Matches 8; Conserv
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Best Local :
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 220 ECC. CITY: San Francisco
STATE: California
Thited State
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lyamichev, Victor I.
APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA
TITLE OF INVENTION: POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP:
                                                                                                                                                                                           Local Similarity hes 8; Conserv
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                                                                                                                           64 FVVFDAKAPSFRH
                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32 REFERENCE/DOCKET NUMBER:
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                                                                                                                                                         7 FVGFDASEPDSRH 19
                                                                                                                                                                                                                                                                                                                                          LENGTH:
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5. 5691142
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                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                                                                            415/397-8338
                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           United States of America
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                                                                                                                                                                                                                                                                                                         single
                                                                                                                           76
                                                                                                                                                                                                           38.1%;
61.5%;
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Pred. No. 2.4e+02;
                                                                                                                                                                                                                          Length 834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 834;
                                                                                                                                                                                             Indels
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APPLICANT:

Gelfand, David H.

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CIP: 07110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,383

FILING DATE:
APPLICATION NUMBER: US/08/384,490

FILING DATE:
APPLICATION NUMBER: US/08/148,133

FILING DATE:
APPLICATION NUMBER: US/08/148,133

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sias, Stacey R.
REGISTRATION NUMBER: 32,630

REFERENCE/DOCKET NUMBER: 8887

TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2863

TELEFAX: (510) 814-2977

INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: Linear

MOLECULE TYPE:
US-08-459-383-31
Search completed: March 27, 2003, 10:07:34 Job time: 5.63415 secs
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                                                                                                                                                             Query Match 38.1%;
Best Local Similarity 61.5%;
Matches 8; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lawyer, Frances C.
APPLICANT: Stoffel, Susanne
TITLE OF INVENTION: Recombinant Expression Vectors and
TITLE OF INVENTION: Purification Methods for Thermus Thermophilus DNA
TITLE OF INVENTION: Polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 340 K
CITY: Nutley
STATE: New Je
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                                                                                     64 FVVFDAKAPSFRH 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hoffmann-La Roche Inc.
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                                                                                                                                                                Score 40; DB 1; Length 834
Pred. No. 2.4e+02;
0; Mismatches 5; Indels
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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AAW53568
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AAW57817417
AAB98659
AAW57887
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                    Cucumber raffinose
Cucumber raffinose
Cucumber raffinose
Cucumber raffinose
Soybean protein: S
Soybean raffinose
Amino acid sequenc
Soybean raffinose
Broad bean raffino
                                                                                                                                                                                                                                                                    Description
  Amino acid sequenc
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Mouse ischaemic co		23	283		40
þ	AAG82256	22	232	38.1	40
Ω,	ABG20734	22	146		40
Human breast tumou	AAY48481	20	145		40
Human normal ovari	AAY59807	20	144		40
Human bone marrow	AAM00853	22	129		40
ionibac	AAU47171	22	78	8	40
l human	ABG01021	22	52	38.1	40
Novel human diagno	ABG01020	22	52	ω.	40
Human polypeptide	AAO10988	22	48	38.1	40
Novel human diagno	ABG19520	22	823	9	41
	AAW82685	20	212	9	41
cumberlandia	AAW82678	20	212	9	41
	AAW82677	20	212	.9	41
um g	AAB76725	22	382	0	42
	AAG90340	22	382		42
rphyrinoge	AAR94460	17	257		42
secreted p	AAY13176	20	22	0.	42
_	AAY70981	21	841		42.5
Ø	AAG15496	21	447	۲	43
B	AAY40501	20	441	1	
gan	AAB50675	22	313	1.	43
റ	ABP31035	23	86	1.	
la melano	ABB60476	22	428	1.	44
	ABB63148	22	421	1.	44
icus bispor	AAW08433	18	112	1.	44
~	AAY70977	21	763	۲.	45
dall	ABB93664	23	783	٠.	5
finos	AAY32074	20	777	٠	46.5
	AAG16863	21	295	٠	47
	AAG16864	21	253	٠	47
idopsis thal	AAG16865	21	175	٠	47
finose sy	AAY70976	21	770	ა	47.5
arbeet raffin	AAY32073	20	783		61
Soybean raffinose	AAY70978	21		59.0	62

ALIGNMENTS

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	,	Example 2; Page 17; 26pp; Japanese.	transformed plant	Raffinose synthase gene - useful for preparation of raffinose in		WPI; 1998-264858/24.		(AJIN) AJINOMOTO KK.		26-APR-1996; 96JP-0107682.			28-APR-1997; 97JP-0111124.		07-APR-1998.		JP10084973-A.		Cucumis sativus.		Cucumber; raffinose synthase; sucrose; galactinol.		Cucumber raffinose synthase residues 61 to 79.		06-JUL-1998 (first entry)		AAW53568;		AAW53568 standard; peptide; 19 AA.	AAW53568	

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The present sequence is a cucumber raffinose synthase fragment.

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RESULT 3
AAW53570
ID AAW5
XX
AC AAW5
XX
DT 06-J
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AAY17423
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Matches 19
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                                                                                                                                                                  The present invention describes a raffinose synthase, having an activity of forming raffinose from sucrose and galactinol. The raffinose synthase gene can be used for expression in a plant for the production of raffinose. The raffinose synthase can give raffinose from sucrose and galactinol efficiently. The present sequence represents a raffinose synthase can give raffinose from sucrose and galactinol efficiently.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Raffinose synthase forms raffinose from sucrose and galactinol, he an optimum pH of 6 to 8 and working temperature of 35 to 40 degree C, has a molecular weight of 75 to 95 kDa by gel filtration or 90 to 100 kDa by PAGE and SDS-PAGE under reductive conditions and is inhibited by iodoacetamide, N-ethylmaleimide and myoinositol.
  06-JUL-1998
                   AAW53570;
                                   AAW53570
                                                                                                                                              Sequence
                                                                                                                                                                                                                                      sucrose and
                                                                                                                                                                                                                                                               WPI; 1999-340516/29
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                                                                                                                                                                                                                                                                                                                                                                                               Cucumber raffinose synthase peptide SEQ
                                                                                                                                                                                                                    Example 2; Page 21; 37pp; Japanese.
                                                                                                                                                                                                                                                                                               24-OCT-1997;
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                                                                                                                                                                                                                                     raffinose synthase gene -
rose and galactinol
                                                                                    PVSVGCFVGFDASEPDSRH 19
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                                                                            PVSVGCFVGFDASEPDSRH 19
                                   standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide;
                                   Protein;
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Pred. No. 2.6e-10;
; Mismatches 0;
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Query Match
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Matches 19
                                 WPI; 1999-340516/29
N-PSDB; AAX61238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is cucumber raffinose synthase, which forms raffinose from sucrose and galactinol, has an optimum 6 to 8 and working temperature of 35 to 40 degrees C, has a molecular weight of 75 to 95 kDa by gel filtration or 90 to by PAGE and SDS-PAGE under reductive conditions and is inhib
                                                                                                                                                                                                                        JP11123080-A.
                                                                                                                                                                                                                                                        Cucumis sativus
                                                                                                                                                                                                                                                                                                                          Cucumber raffinose
                                                                                                                                                                                                                                                                                                                                                                                           AAY17417;
                                                                                                                                                                                                                                                                                                                                                                                                                            AAY17417 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Raffinose synthase gene - useful for preparation transformed plant % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right\} 
 New raffinose synthase
                                                                                   (AJIN ) AJINOMOTO KK
                                                                                                                     24-OCT-1997;
                                                                                                                                                      24-OCT-1997;
                                                                                                                                                                                                                                                                                       Raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                         29-JUL-1999
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26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cucumber; raffinose
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                                                                                                                                                                                       11-MAY-1999.
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                                                                                                                      97JP-0292969
                                                                                                                                                      97JP-0292969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97JP-0111124
                                                                                                                                                                                                                                                                                                                        synthase
                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                         sucrose;
                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthase; sucrose; galactinol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
gene -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19
                                                                                                                                                                                                                                                                                                                                                                                                                            784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                         galactinol
   for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 105; DB 19;
Pred. No. 1.2e-08;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                            AΑ
 production of raffinose from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is inhibited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 kDa
bited by
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Best Local
                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                   Query Match
                                                                                                                          The present invention relates to a mutant protein of raffinose synthase in which at least one aromatic amino acid present at the position of about 1-7 amino acids from the N-terminus is deletted or replaced. The mutant protein can be used for reducing the raffinose oligosaccharide content in a plant body. The present protein from soybean, was used in the present protein from soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a raffinose synthase, having an activity of forming raffinose from sucrose and galactinol. The raffinose synthase gene can be used for expression in a plant for the production of raffinose. The raffinose synthase can give raffinose from sucrose and galactinol efficiently. The present sequence represents raffinose
                                                                                           Sequence
                                                                                                                                                                                                                          Novel mutant protein of raffinose synthase is useful for raffinose oligosaccharide content in a plant body -
                                                                                                                                                                                                                                                                          WPI; 2001-313373/33.
                                                                                                                                                                                                                                                                                                                           09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                 03-JUL-2000; 2000JP-0200571.
                                                                                                                                                                                                                                                                                                                                                                                                 JP2001078783-A
                                                                                                                                                                                                                                                                                                                                                                                                                       Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                                              plant; soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mutant; mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soybean protein:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB98659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB98659 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synthase from cucumber.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2;
                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                N-PSDB; AAH27438.
                                                                                                                                                                                                                                                                                                                                                                          27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-AUG-2001
                                                                                                                                                                                                                                                                                                  (SUMO ) SUMITOMO CHEM
68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                         Local
                      4 VGCFVGFDASEPDSRH 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 PVSVGCFVGFDASEPDSRH 19
                                                                                                                 present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVSVGCFVGFDASEPDSRH 79
VGCFVGFHADEPRSRH
                                              l Similarity
13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  784 AA;
                                                                                           780 AA;
                                                                                                                                                                                                    Page 18-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-27; 37pp; Japanese
                                                                                                                                                                                                                                                                                                                           99JP-0196036
                                                                                                                                                                                                                                                                                                                                                                                                                                                          raffinose synthase; raffinose oligosaccharide reduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                         67
81
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                                                         26
                                                                                                                                                                                                 30pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        780
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                                             0;
                                                         Score 71;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 105; DB 20;
Pred. No. 1.2e-08;
; Mismatches 0;
                                                                                                                                                                                                    Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                              Mismatches
                                                         DB 22;
                                                                  Length 780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         784;
                                                                                                                                                                                                                                       reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                             0;
                                           Gaps
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                                             0;
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RESULT

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RESULT 7
AAY30143
ID AAY3
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ID AAW5
PD XXX
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                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                  This sequence represents the soybean raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides in the host organism or cell is changed. Raffinose oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 31-34; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-324670/29
N-PSDB; AAV40801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oeda K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Raffinose synthetase; metabolism gastrointestinal flora; soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Soybean raffinose synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW57887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW57887 standard; Protein; 781 AA
                      JP11215984-A.
                                             Glycine max.
                                                                   Raffinose synthase; plant;
                                                                                           Amino acid sequence of a raffinose synthase protein.
                                                                                                                                                                    AAY30143 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-1997;
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                                                                                                                     26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                89
                                                                                                                                                                                                                                                     4 VGCFVGFDASEPDSRH 19
                                                                                                                                                                                                                            VGCFVGFHADEPRSRH
                                                                                                                                                                                                                                                                              l Similarity
13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wantanabe
                                                                                                                                                                                                                                                                                                                               781 AA;
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96JP-0338673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97EP-0122417
                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                         67.6%;
81.2%;
                                                                                                                                                                                                                                83
                                                                      sucrose;
                                                                                                                                                                   781 AA
                                                                                                                                                                                                                                                                                        Score 71;
Pred. No.
                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modification;
                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                        DB 19;
0.0044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            food additive;
                                                                                                                                                                                                                                                                                                   Length 781;
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         raffinose by
                                                                                                                                                                                                                                                                               0
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RESULT 8
AAB49400
ID AAB4
XX AAB4
AC AAB4
XX Plan
DT 07-M
XX Plan
XX IShi
XX I
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Best Local S
Matches 13
  Sequence
                                                                                                                                          Example 6; Page 24-27;
                                                                                                                                                                                                  with
                                                                                                                                                                                                    New soybean plant promoters useful for generating transgenic plants with desired properties -
                                                                                                                                                                                                                                                                                                                                                                                                                                            30-APR-1999;
01-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1048733-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Soybean raffinose synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB49400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB49400 standard; Protein; 781 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a raffinose synthase protein. The sequence is isolated from plant material. The protein forms raffinose by complexing alpha(1 to 6)- D-galactosyl hydroxyl group of the 6C of D-glucose residue in sucrose molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Page 25-27; 40pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAZ10002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-APR-2000; 2000EP-0108962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New raffinose synthase gene - is prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-511112/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-NOV-1997;
18-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                             Ishige F,
                                                                                                                                                                                                                                                                                                                                                                                            (SUMO ) SUMITOMO CHEM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 VGCFVGFDASEPDSRH 19
                                                                    present invention provides novel plant promoters which can production of transgenic plants which express genes with \ensuremath{\mathrm{d}} \epsilon
                                                                                                                                                                                                  desired
                                                                                                                                                                                                                                                                                               2001-104537/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGCFVGFHADEPRSRH 83
                                                                                                                                                                                                                                                                        AAC89523
                                                                                                                                                                                                                                                                                                                                             Watanabe
     781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          781 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                             properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
     AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-0124527.
99JP-0247211.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96JP-0338673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97JP-0342899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transgenic plant; desired property.
                                                                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.6%;
81.2%;
                                                                                                                                             36pp; English
                                                                                                                                                                                                                                                                                                                                               0eda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 71;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 20;
0.0044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plant material
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                         an be used
desired
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                                                                                                  in
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Query Match

67.6%;

Score

71;

DΒ

22;

Length 781;

26-OCT-1999

(first entry)

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RESULT 10
AAY30142
ID AAY30
XX
AC AAY30
XX
AC AAY30
XX
XX
XX
XX
DT 26-OC
XX
                                                                                                                                                                                                                      RESULT 9
AAW57886
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                                                                                                                                                                     Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                         This sequence represents the broad bean raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
                                    AAY30142;
                                                           AAY30142 standard;
                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 26-29; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oeda K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW57886 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAV40800
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-324670/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP849359-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vicia faba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gastrointestinal flora; broad bean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raffinose synthetase; metabolism modification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Broad bean raffinose synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW57886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SUMO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-1997;
                                                                                                                       87
                                                                                                                                                                      Local Similarity
nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                              S
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                                                                                                                                              GCFVGFDASEPDSRH 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGCFVGFHADEPRSRH 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VGCFVGFDASEPDSRH 19
                                                                                                                      GCFVGFNSTEPKSHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMITOMO CHEM CO LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wantanabe
                                                                                                                                                                                                                     799 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96JP-0338673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97EP-0122417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ħ
                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                   60.0%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            799
                                                             799 AA
                                                                                                                                                                                  Score 63;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.0044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ĀΑ
                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                  DB 19;
0.092;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             food
                                                                                                                                                                                              Length 799;
                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             additive;
                                                                                                                                                                      0;
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                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a raffinose synthase protein. The sequence is isolated from plant material of broad beans. The protein forms raffinose by complexing alpha(1 to 6)- D-galactosyl hydroxyl group of the 6C of D-glucose residue in sucrose molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New
Nucleic acids and encoded proteins involved in the biosynthesis of raffinose, useful for producing soybean seeds with a reduced raffinose content and therefore improved nutritional quality -
                                                                                                       23-OCT-1998;
                                                                                                                         22-OCT-1999;
                                                                                                                                           04-MAY-2000
                                                                                                                                                              WO200024915-A2
                                                                                                                                                                               Glycine max.
                                                                                                                                                                                                Soybean; raffinose synthase; clone sfl1.pk125.d4; nutrition
                                                                                                                                                                                                                           Soybean raffinose synthase
                                                                                                                                                                                                                                               09-AUG-2000
                                                                                                                                                                                                                                                                                   AAY70978 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 19-21; 40pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-511112/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-NOV-1997;
18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP11215984-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vicia faba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino
                                                                                   (DUPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-AUG-1999
                                                                                                                                                                                                                                                                                                                                 87
                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                 5 GCFVGFDASEPDSRH 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         raffinose synthase gene - is prepared
                                       2000-350754/30
DB; AAD00335.
                                                                                                                                                                                                                                                                                                                                 GCFVGFNSTEPKSHH 101
                                                                                                                                                                                                                                                                                                                                                                     1 Similarity
10; Conserv
                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ10001
                                                                 Hitz
                                                                                   PONT DE NEMOURS &
                                                                                                                                                                                                                                                                                                                                                                                                          799 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97JP-0329006.
96JP-0338673.
                                                                                                      98US-0105451
                                                                                                                         99WO-US24923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97JP-0342899
                                                                  ₩D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of.
                                                                                                                                                                                                                                                                                                                                                                             60.0%;
                                                                                                                                                                                                 nutritional;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 raffinose synthase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 broad
                                                                                                                                                                                                                            from clone sfll.pk125.d4
                                                                                                                                                                                                                                                                                   758 AA
                                                                                                                                                                                                                                                                                                                                                                    Score 63; DB Pred. No. 0.09
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     ω
••
                                                                                    ဗ
                                                                                                                                                                                                           raffinose saccharide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bean; sucrose;
                                                                                                                                                                                                 soy protein
                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                               .092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from a
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                                                                                                                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plant
                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                       799;
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RESULT 12
AAY32073
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Best Local s
Matches 1
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30-APR-1998;
04-DEC-1998;
10-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a raffinose synthase from clone sfl1.pkl25.d4 isolated from a soybean immature flower cDNA library sfl1. Raffinose synthase is involved in the blosynthesis of raffinose and higher homologues in the raffinose saccharide family from sucrose. The present sequence is useful for reducing the raffinose saccharide content of soybean seeds which improves the nutritional quality of the soy protein products derived from them.
          This sequence represents sugarbeet raffinose synthase, a protein that can bind a D-galactosyl group through an alpha(1-6) bond to thydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. cDNA (see AAZ20208) encoding the enzyme was isolated from sugarbeet contaming leaf cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see AAZ20207-10) may be used to obtain
                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sugarbeet raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY32073 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                            raffinose
                                                                                                                                                             N-PSDB; AAZ20208
                                                                                                                                                                                                Watanabe
                                                                                                                                                                                                                                                                                                   27-APR-1999;
                                                                                                                                                                                                                                                                                                                         03-NOV-1999
                                                                                                                                                                                                                                                                                                                                               EP953643-A2
                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                        Beta vulgaris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY32073;
                                                                                                                                                                                                                    (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 TTGCFLGFHATSPKSRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      w
                                                                                                                           sense and antisense genes, useful finose in food plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVGCFVGFDASEPDSRH
                                                                                                                                                                         1999-593144/51.
 raffinose synthase genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Page 47-49;
                                                                                                    25; Page 22-24; 55pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
10; Conser
                                                                                                                                                                                               Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          758 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                             Oeda K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                          98JP-0120550.
98JP-0120551.
98JP-0345590.
98JP-0351246.
                                                                                                                                                                                                                                                                                                   99EP-0107430
                                                                                                                                                                                                                                                                                                                                                                                  348
                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 227
                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                          'note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                             sugarbeet;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.0%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19
                                                                                                                                                                                                                                                                                                                                                                     "encoded by CCR"
                                                                                                                                                                                                                                                                                                                                                                                           "encoded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         783
                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 62; [
Pred. No. 0.
 γģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                             transgenic plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
labeled detection
                                                                                                                                                                                                                                                                                                                                                                                           CCM,
                                                                                                                                       for altering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                       the
 amplification
                                                                                                                                       level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                       Q,
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                                                                    the
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RESULT 13
AAY70976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                 The present sequence is a raffinose synthase from clone rls24 pk0017,g10 isolated from a rice infected leaf cDNA library rls24. Raffinose synthase is involved in the biosynthesis of raffinose and higher homologues in the raffinose saccharide family from sucrose. The present sequence is useful for reducing the raffinose saccharide content of soybean seeds which improves the nutritional quality of the soy protein products derived from them.
                                                                                                                    Claim 2; Page 40-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rice;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (claimed). These genes may be used to control the levels of raffinose produced in plants. Antisense genes can be used to knock out existing gene activity, and sense genes to increase the level of gene activity. The resulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, providing general health advantages.
Sequence
                                                                                                                                         Nucleic acids and encoded proteins involved in the biosynthesis of raffinose, useful for producing soybean seeds with a reduced raffinose content and therefore improved nutritional quality -
                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                               04-MAY-2000.
                                                                                                                                                                                                                                Allen
                                                                                                                                                                                                                                                      (DUPO)
                                                                                                                                                                                                                                                                              23-OCT-1998;
                                                                                                                                                                                                                                                                                                      22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                      WO200024915-A2
                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY70976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY70976 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 GCFVGFDASEPDSRH 19
                                                                                                                                                                                            2000-350754/30.
DB; AAD00333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLFVGFDAPEPKARH 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               raffinose synthase; raffinose saccharide; rls24.pk0017.g10; nutritional; soy protein
                                                                                                                                                                                                                                                       DQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                               Hitz WD;
                                                                                                                                                                                                                                                      PONT DE
770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    783 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
AA,
                                                                                                                                                                                                                                                                              98US-0105451
                                                                                                                                                                                                                                                                                                      99WO-US24923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthase from clone
                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 100..101
                                                                                                                                                                                                                                                                                                                                                                                                    represented 101..110
                                                                                                                                                                                                                                                                                                                                                                                        /label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Encoded by a
                                                                                                                                                                                                                                                      NEMOURS & CO E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.1%;
73.3%;
                                                                                                                  58pp; English.
                                                                                                                                                                                                                                                                                                                                                                           770
                                                                                                                                                                                                                                                                                                                                                                                                             as base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 61;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                      Ħ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rls24.pk0017.g10
                                                                                                                                                                                                                                                                                                                                                                                                            region of 105 nucleotides
pairs 693-797 in AAD00333"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               soy protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             soybean;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                             the raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Query Match

45

. 28;

Score

47

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DВ

21;

Length

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RESULT 14
AAG16865
ID AAG16665
XX AAG166
XX AAG166
XX DT 17-OC
XX Prote
KW Prote
KW Prote
KW Prote
KW Prote
XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity Matches 11; Conserv
20-MAY 1999;
21-MAY 1999;
24-MAY 1999;
25-MAY 1999;
27-MAY 1999;
28-MAY 1999;
01-JUN 1999;
01-JUN 1999;
07-JUN 1999;
08-JUN 1999;
10-JUN 1999;
10-JUN 1999;
10-JUN 1999;
10-JUN 1999;
10-JUN 1999;
                                                                                                                                                                                                                                                                                                                                                         30-APR 1999
30-APR 1999
04-MAY 1999
05-MAY 1999
06-MAY 1999
06-MAY 1999
07-MAY 1999
11-MAY 1999
14-MAY 1999
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29-MAR-1999;
01-APR-1999;
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23-APR-1999;
                                                                                                                                                                                                                                                                               19-MAY-1999
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14-MAY-1999;
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21-APR-1999;
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ALIGNMENTS

3-phosphoserine phosphatase [imported] - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C.Accession: B86320
C.Accession: B86320
C.H., C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marzia A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Mu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Ritle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712 C;Accession: AF3233
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; erage, G; Gillet, W.; Grant, C.; Guenthmer, D.; Kutyavin, T.; Levy, R.; Li, M.; Y.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001 conserved hypothetical protein Atu6048 [imported] - Agrobacterium tumefaciens C:Species: Agrobacterium tumefaciens C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002 RESULT B86320 A; Genome: plasmid C; Superfamily: Lactococcus lactis hypothetical protein PL08712.1A;Reference number: AB2577; PMID:11743193
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A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-836 <KUR>
A;Residues: 1-836 <KUR>
A;Cross-references: GB:AE008690; PIDN:AAL46284.1; PID:917744066; GSPDB:GN00189 A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A; Reference number: AB2577; PMID:11743193A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam ster, E.W. В δ C; Genetics: A; Gene: Atu6048 A; Experimental source: strain C58 (Dupont) A; Accession: B86320 Query Match Best Local Matches 687 NLGAYLGFDAERPEAVH 703 N Local Similarity es 7; Conserv 3 SVGCFVGFDASEPDSRH 19 Conservative 46.7%; Pred. No. Score 49; Mismatches σ DB 2; 4; Indels Length 836; 0 Gaps 0: (strain MCC1

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-295 <STO>
A;Cross references: GB:
C;Genetics:
A;Map position: 1
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A;Pathway: serine biosynthesis (plastidic pathway)
C;Keywords: chloroplast; phosphoric monoester hydrolas
                                                   A:Map position: circular chromosome C;Superfamily: Haemophilus influenza
                                                                                                                                                                                        A; Reference number: A97359; A; Accession: A97544
                                                                                                                                                                                                                                         R;Goodner, B.; Hinkle, G.; G
A.; Liu, F.; Wollam, C.; Al
Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                         C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                              οy
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J. Biol. Chem. 274, 11007-11012,
A;Title: Plastidic pathway of sea
A;Reference number: Z25385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Arabidopsis thallana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000
C;Accession: T51362
                                                                                      A; Gene: AGR_C_2794
                                                                                                                       A; Residues: 1-336 < KUR>
A; Cross-references: GB:
                                                                                                                                                                                                                                                                                           C; Accession: A97544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphoserine phosphatase (EC 3.1.3.3) precursor,
N;Alternate names: 3-phosphoserine phosphatase
C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                          A; Title: Genome Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Function
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A; Residues: 1-295 < HOC>
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                   Query Match
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                                                                                                                                                                                                                                                                                                                                       family protein VC0379 [imported] - Agrobacterium tumefaciens (strain
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9; Conserv
   Similarity.
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                                                                                                                       GB: AE007869;
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                                                                                                                                                                                                                                                         G.; Gattung, S.;
C.; Allinger, M.;
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   44.8%;
47.1%;
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64.3%;
                                                 influenzae conserved hypothetical protein
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                                                                                                                     PIDN: AAK87306.1;
   Score
Pred.
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Pred. No.
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Pred.
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                                                                                                                                                                                                                                                         Miller, N.; Blanchard, M.; Quro Doughty, D.; Scott, C.; Lappas,
   47;
No.
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4.8;
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DB
3.5;
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                                                                                                                     PID:g15156601;
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                                                                                                                     GSPDB:GN00169
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Markelz, B.
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GTP-binding protein [C;Species: Brucella mC;Date: 01-Feb-2002 #C;Accession: AH3445
                             Ωy
                                                                                                                             C; Superfamily: Mycobacterium leprae probable GTP-binding protein;
                                                                                                                                                                                                             A; Cross-references: GB:AE008917; PIDN:AAL52731.1; PID:g17983561; GSPDB:GN00190
                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-483 < KUR>
                                                                                                                                                                                                                                                                           R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; L.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Call Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen A;Reference number: AD3252; PMID:11756688
Ъ
                                                                                                                                               A; Map
                                                                                                                                                               A; Gene: BMEI1550
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                                                                                                                                                                                                                                                             A; Status: preliminary
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C; Superfamily: F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: AB2763
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D., erage, G.; Gillet, W.; Grant, C.; Guenthner, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE008688; PIDN:AAL42520.1; A;Experimental source: strain C58 (Dupont)
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A; Residues: 1-336 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Authors: Yoo, H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein Atu1515 [imported] -
C; Species: Agrobacterium tumefaciens
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184
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                             PVSVGCFVGFDASEPDS 17
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8; Conserv
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Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                               [imported] - Brucella melitensis (strain
melitensis
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47.18;
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                                                                              43.8%;
47.1%;
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Pred.
                                                                              Pred. No.
                                                                                            Score 46;
                                                               Mismatches
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12;
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5.5;
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                                                                                              Length 483
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T.; Levy, R.; Li,
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O'Callaghan,
                                                             0;
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D.; Let
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C;Species: Agaricus bisporus (cultivated mushroom)
C;Date: (06-Dec-1996 #sequence_revision (07-Feb-1997 #text_change 21-Jul-2000
C;Accession: S68584, S66586; S58342
R;de Groot, P.W.J.; Schaap, P.J.; Sonnenberg, A.S.M.; Visser, J.; van Griensven, L.J.L.
J. Mol. Biol. 257, 1008-1018, 1996
A;Title: The Agaricus bisporus hypA gene encodes a hydrophobin and specifically accumul A;Reference number: S68584, MUID:96192085; PMID:8632464
A;Accession: S68584
                C;Accession: A43741
R;Baldarelli, R.M.; Mahoney, P.A.; Salas, F.; Gustavson, E.;
Dev. Blol. 125, 85-95, 1988
A;Title: Transcripts of the Drosophila blastoderm-specific lo
A;Reference number: A43741; MUID:88055884; PMID:3334721
A;Accession: A43741
                                                                                                                                                                                                                         RESULT 9
A43741
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                                                                                                                                                    terminus protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 04-Mar-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-301 <SMI>
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A; Accession: S73023
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C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type:
A; Residues: 1-11
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A; Residues: 1-112 <DEG>
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Best Local :
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preliminary
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Similarity 46.28;
6; Conservation
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                41.9%;
57.1%;
                                          Drosophila blastoderm-specific locus, MUID:88055884; PMID:3334721
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Pred. No. 15;
1; Mismatches
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A; Molecule type: mRNA
A; Residues: 1-650 <HOR>
A; Residues: 1-650 <HOR>
A; Cross-references: GB: M91599; NID: g204137; PIDN: AAA41157.1;
R; Lai, C; Lemke, G.
Neuron 6, 691-704, 1991
Neuron 6, 691-704, 1991
A; Title: An extended family of protein-tyrosine kinase genes
A; Reference number: PT0183; MUID: 91222580; PMID: 2025425
A; Accession: PT0191
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C;Genetics:
A;Gene: FlyBase:term
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C;Superfamily: Drosophila terminus prot
C;Keywords: DNA binding
                       C; Function:
                                        A; Gene:
                                                               C; Genetics:
                                                                                A; Experimental source:
                                                                                                   A; Molecule type: mRNA
A; Residues: 465-518 <LAI>
                                                                                                                                                                                                                                                                                                     A; Reference number: JC1450; A; Accession: JC1450
                                                                                                                                                                                                                                                                                                                            A; Title: Cloning, expression and tissue distribution of A; Reference number: JC1450; MUID:93013049; PMID:1398143
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R; Horlick, R.A.; Stack, S.L
Gene 120, 291-295, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 01-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                               fibroblast growth factor receptor 4 - rat
N;Contains: protein-tyrosine kinase (EC 2
C;Species: Rattus norvegicus (Norway rat)
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A; Note: T22P11.70
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A;Experimental source: cultivar C
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A; Accession: T48269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein T22P11.70 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 19-May-2000 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 19-May-2000 C:Accession: T48269
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A; Description: receptor mediating effects of fibroblast growth factor
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nes 7; Conserv
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                                                                                                                                                               of protein-tyrosine kinase genes MUID:91222560; PMID:2025425
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Pred. No.
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l; Mismatches
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ced. No. 22;
Mismatches
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April 2000
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712
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F:110-181/Domain: immunoglobulin homology <IM2>
F:218-238/Domain: intracellular *status predicted <INM>
F:313-580/Domain: intracellular *status predicted <INT>
F:313-598/Domain: protein kinase homology <KIN>
F:321-329/Region: protein kinase ATP-binding motif
F:321-329/Region: protein kinase ATP-binding motif
F:104,136,157,168/Binding site: carbohydrate (Asn) (covalent) *status predicted
F:465,478/Binding site: magnesium (Asn, Asp) *status predicted
F:465,478/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein [imported] - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002 C;Accession: F86185
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A: Map position: 5
**Therons: 18/2; 82/3; 117/1; 210/2; 241/3;
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A; Molecule
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A;Residues: 1-313 <MIL>
A;Cross-references: EMBL:AF067937; PIDN:AAC19217.1; GSPDB:GN00023; CESP:F22F7.6
A;Experimental source: strain Bristol N2; clone F22F7
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Best Local
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                      preliminary
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9; Conservery
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Pred. No.
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Biochim. Biophys. Acta 1252, 185-188, 1995
A;Title: Amino-acid sequence of rat liver kynureninase.
A;Reference number: S59898; MUID:96049498; PMID:7578221
A; Residues: 1-464 <TAI
C; Keywords: hydrolase
                                                                      A; Status: preliminary
                                                                                               A; Accession: S59898
                                                                                                                                                                                                  R; Takeuchi, F.; Tsubouchi, R.; Yoshino, M.; Shibata, Y.
                                                                                                                                                                                                                       kynureninase (EC 3.7.1.3) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jul-1996 #sequence_revision 13
C;Accession: S59898
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Best Local Similarity
Thehes 8; Conserve
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A;Molecule type: DNA
A;Residues: 1-447 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: F84733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Mierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, A;Description: Arabidopsis thaliana A;Reference number: Z14678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Cr
submitted to the EMBL Data Library, July 1998
A;Description: Arabidopsis thaliana chromosome II BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999
C;Accession: T02547; F84733
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A;Cross-references: GB:AE005172; NID:g2388583; PIDN:AAB71464.1; GSPDB:GN00141
C;Genetics:
                                              A; Molecule type: protein
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C;Superfamily: Escherichia coli probable zinc proteinase yaeL
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                         1-464 <TAK>
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PERB_PICAN
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p11455 drosophila
p70712 rattus nor
Q18026 caenorhabd
Q8yq64 anabaena s
Q9fmb0 arabidopsi
Q01886 cochliobol
p36827 human papi
p45879 bos taurus
Q9ft15 oryctolagy
Q160932 mus muscul
Q000869 paramecium
Q10719 homo sapit
p19121 gallus gal
Q00925 pichia ang
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Q16797 drosophili
Q99718 clostridi
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Q99718 caulobact
Q43772 homo sapi
Q94716 mus muscu
Q13712 homo sapi
Q94713 herpes sii
p183449 bacillus
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ა 8	38	38	38	38.5	38.5	38.5	38.5	39	39	39	39
36.2	36.2	36.2	36.2	36.7	36.7	36.7	36.7	37.1	37.1	37.1	37.1
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MCAT_RAT	MCAT_MOUSE	CSGD_SALTY	VE7_HPV07	SM5A_MOUSE	SM5A_HUMAN	CP4B_RABIT	VGLL_HSVEB	P152_YEAST	RRPO_ROTS1	RRPO_ROTPG	RRPO_ROTBU
P97521 r	Q9z2z6 m	054294 s	P36816 h	Q62217 m	Q13591 h	P15128 o	P28941 e	P39685 s	P22678 s	P17699 p	
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RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., Hich R.W., Hoskins R.A., Galle R.F.,
RA Adams N.D., Celniker S.E., Hich R.W., Hoskins R.A., Galle R.F.,
RA Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Glerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Chandra I.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew II., Dietz S.M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Ködira C.D., Kraft C., McLeod M.P., McPherson D.L.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Nelson D.R., Nelson K.A., Nixon K., Nussken D.R., Pacleb J.M.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
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Best Local :
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01-OCT-1989 (Rel. 12, Created)
16-OCT-2001 (Rel. 40, Last sequ
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  are
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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TERM OR TER OR CG4216.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7227
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Best Local S
Matches 7
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P70712; Q9QW90;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Kynureninase (EC 3.7.1.3) (L-kynurenine hydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                         Eur.
                                                                                           Alberati-Giani D., Buchli R., Malherbe
Koehler C., Lahm H.-W., Cesura A.M.;
"Isolation and expression of a cDNA clo
                                                                                                                                                                    TISSUE=Liver, and Kidney; MEDLINE=96314506; PubMed=8706755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000822; Znf_C2H2.

PROSITE; BSS0157; ZINC_FINGER_C2H2_2; UNKNOWN_1.

DNA-binding; Zinc-finger; Developmental protein.

ZN_FING 325 346 C3H-TYPE.

ZN_FING 325 346 C3H-TYPE.

ZN_FING 325 346 C3H-TYPE.

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-i- DEVELOPMENTAL STAGE: EXPRESSED FROM THE CELLULAR BLASTODERM STON, MOST DURING GASTRULATION AND IS NO LONGER DETECTED BY THE
                                                                    "Isolation and expression kynureninase.";
                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                 Toma
                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takeuchi F., Tsubouchi R., Yoshino M., Shibata "Amino-acid sequence of rat liver kynureninase. Biochim. Biophys. Acta 1252:185-188(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blochim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Wistar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KYNU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97324088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96049498; PubMed=7578221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                              "Cloning
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                    . J. Biochem. 239:460 FUNCTION: CATALYZES
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S
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                                                                                                                                                                                                                                                                       and recombinant expression t. 408:5-10(1997).
                                                                                                                                                                                                                                                                                                                                         Nakamura M.,
                                                                                                                                                                                                                       OF 19-117 FROM
                                                                                                                                                                                                                                                                                                                  akamura M., Tone S., Oku
Cozzi L., Speciale C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         428 AA;
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                                                  239:460-468(1996)
                                                                                                                                                                                                                                                                                                                                                                        PubMed=9180257;
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50.0%;
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                      THE
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; F545653F738AE434 CRC64;
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Pred. No.
                                                                                                                                                                                                                       AND
                                                                                                                                                                                                                                                                                                                       Okuno E., Kido R., Breton J.,
C., Mostardini M., Gatti S., E
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                                                                                                                                                                                                                       PARTIAL SEQUENCE
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  OF L-KYNURENINE
ANTHRANILIC (A)
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                                                                                                encoding
                                                                                                                                                                                                                                                                                                 and human kynureninase.
                                                                                                                                              Broger C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Usage
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INE (L-KYN) AND L-3-
(AA) AND 3-
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                                                                                                                                                                                                                                                                                                                       Benatti L.;
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HE END
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Best Local
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                                                                                                                                                                                                                                                                                                                                        CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
CONFLICT
                   KOhara Y., Shin'i T., Suzuki Y., Sugano S., Potdevin M., Kohara Y., Shin'i T., Suzuki Y., Sugano S., Potdevin M., Thierry-Mieg J.; Thierry-Mieg J.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases -- CATALYTIC ACTIVITY: L-kynurenine + H(2)0 = anthrani.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
                                                                                                                                                                                                                                                                                                                            KYNU_
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                                                                               STRAIN-Bristol
                                                                                           SEQUENCE FROM N.A.
                                                                                                                      Submitted
                                                                                                                                    Bentley
                                                                                                                                                STRAIN-Bristol
                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                      Eukaryota; Metazoa;
Rhabditidae; Peloder
                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                               C15H9.7
                                                                                                                                                                                                                                                          Probable kynureninase
                                                                                                                                                                                                                                                                     15-DEC-1998 (Rel. 37,
15-DEC-1998 (Rel. 37,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                018026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U68168; AAC53206.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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CATALYTIC ACTIVITY: L-3-hydroxykynurenine + H(2)0 = 3-hydroxyanthranilate + L-alanine.

COFACTOR: PYRIDOXAL PHOSPHATE.

ENZYME REGULATION: INHIBITED BY O-METHYLBENZOYLALANINE PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF NAD COFACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYDROXYANTHRANILIC ACIDS (3-OHAA), RESPECTIVELY. HAS A PREFER FOR THE L-3-HYDROXY FORM. DETIMUM ACTIVITY IS AROUND PH 9.0 F KYN AND AROUND 8.5 FOR L-3OHKYN. ALSO HAS CYSTEINE-CONJUGATE-BETA-LYASE ACTIVITY.

CATALYTIC ACTIVITY: L-kynurenine + H(2)0 = anthranilate + L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European Bioinformatics Institute. The by non-profit institutions as long ifled and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: HIGH LÉVELS IN LIVER AND KIDNEY. ALSO DETECTED IN HEART, RETINA, OVARY. LUNG, TESTIS AND BRAIN. INDUCTION: INHIBITED BY THIOL REAGENTS AND HEAVY METAL IS SIMILARITY: BELONGS TO THE KYNURENINASE FAMILY. SLIGHTLY
 alanine.
COFACTOR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRYPTOPHAN THROUGH THE KYNURENINE PATHWAY.
                                                                                                                                                                                                                                                                                                                           CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                      (MAY-1996)
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276
18
26
118
118
464 AA;
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                                                                                                                                                                                                                                                                                                                                                                                               250
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                                                                                                                                                                                                      Peloderinae;
 PYRIDOXAL
                                                                                                                                                                                                                                                                                                                            STANDARD;
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18
26
118
52453
                                                                                                                                                                                                      Nematoda; Chromadorea; Rhabditida; Rhabditoidea; inae; Caenorhabditis.
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100.0%;
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                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
(EC 3.7.1.3) (L-kynurenine hydrolase)
                                                                                                                                                                                                                                                                                                  Created)
PHOSPHATE
                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW.
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                                                                                                                      EMBL/GenBank/DDBJ databases
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Pred. No.
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D -> N (IN REF. 1).
T -> S (IN REF. 1).
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PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                            PRT;
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(BY
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14;
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                          anthranilate
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SLIGHTLY RELATED
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RESULT 5
Y3H1_ANASP
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Best Local
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QBYQ64;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last seq
15-JUN-2002 (Rel. 41, Last ann
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Hydrolase; Pyridoxal phosphate.
BINDING 289 289 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SEQUENCE 478 AA; 54049 MW; E889450929EC94BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                          cyanobacterium Anabaena sp. strain DNA Res. 8:205-213(2001).
-i- COFACTOR: Zinc (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U56965; AAB52668.1; -. EMBL; AF303267; AAG50225.1; -. WormPep; C15H9.7; CE06835.
                                        InterPro; IPR001478; InterPro; IPR004387; InterPro; IPR000130;
                                                                                      MEROPS;
                                                                                                  EMBL; AP003594; BAB75670.1;
                                                                                                                                                                                                                                                                                                                                                                                                                Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=21595285; PubMed=11759840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Cyanobacteria; Nostocales; NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anabaena sp. (strain PCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALL3971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical zinc
                                                                                                                                                                                                                                                  -!- SIMILARITY: CONTAINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: BELONGS TO THE KYNURENINASE FAMILY. SLIGHTLY RELAT
TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO PEPTIDASE FAMILY M50B SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                (By similarity).
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41, Last annotation update)
metalloprotease All3971 (EC
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
15;
                                                                                                                                                                                                                                                                                            protein.
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                                                                                                                                                                                                                                                                                               Inner membrane
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MBL outstation -
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Pfam; PF00595; PDZ;

Zn_MTpeptdse

SM00228;

TIGR00054;

mem_zinc_metalprot;

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RESULT 6
GL19_ARATH
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                                                                                                                                 RX MEDLINE=21016721; pubmed=11130714;

RX MEDLINE=21016721; pubmed=11130714;

RA MIyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,

RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,

RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,

RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,

RA Miyajima N., Sasamoto S., Kimura S., Shinpo S., Takeuchi C., Wada T.,

RA Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S.,

RA Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,

RA Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,

RA Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,

RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,

RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,

RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,

RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,

RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,

RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,

RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,

RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strowmatt C.,

RA Wagner-McPherson C., Wollam A., Yoakum M., Bell M., Dedhia N.,

RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,

RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,

RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,

RA Kirchoff K., Toth K., King L., Bahret A., Stiekema W., Pohl T.,

RA Kirchoff K., Toth K., King L., Bahret A., Stiekema W., Pohl T.,

RA Kirchoff K., Toth K., King L., Bahret A., Stiekema W., Pohl T.,

RA Kirchoff K., Mambutt R., Duesterhoeft A., Stiekema W., Pohl T.,

RA Kirchoff K., McCullagh B., Robben J., Grymonprez B., Zimmermann W.,

RA Kansperger U., Wedler H., Bolke K., Wedler E., Peters S.,

RA Van Staveren M., Dixkse W., Mooljan P., Klein Lankhorst R.,

Ra Kirchoff H., School H., Klein Lankhorst R.,

Ra Kirchoff M., Lamberth 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 8
Sato S.,
Tabata S.
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative germin-like protein subfamily 1 member 9 precursor AT5638910 OR K15E6.14 OR K15E6_90.
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                                   MEDLINE=98290546; PubMed=9628582
                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
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4EM 281

MEM 92

4EM 281

1EM 329

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10 364 AA;
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                                                                                                         408:823-826(2000).
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PS00142;
                Kaneko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Columbia;
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; 54F6AAE818AEFBEA CRC64;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZINC (CATALYTIC) (POTENTIAL)
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POTENTIAL.
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                Miyajima
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Best Local
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Q01886;

Q1-FEB-1994 (Rel. 2

Q1-FEB-1994 (Rel. 2

Q1-FEB-1994 (Rel. 2

15-JUN-2002 (Rel. 4

HC-toxin synthetase
                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-ATCC 90305 / SB111;
MEDLINE-93100328; Pubbed-1281482;
Scott-Craig J.S., Panaccione D.G., Pocard J.-A., Walton
"The cyclic peptide syntherase catalyzing HC-toxin produ
filamentous fungus Cochliobolus carbonum is encoded by a
15.7-kilobase open reading frame.";
J. Biol. Chem. 267:26044-26049(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                   HTS1
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota;
Pleosporales; Pleosporaceae;
                                                                                                                                                                                                                                                                                                                                                                                        Cochliobolus carbonum (Bipolaris zeicola)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _COCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
METAL
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STRAIN=ATCC 90305
MEDLINE=20138231;
                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00325; GERMIN.
PROSITE; PS00725; GERMIN; 1.
Apoplast; Cell wall; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB009048; BAI
HSSP; P45850; 1FI2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA RES. 5:41-54(1998).

-i- FUNCTION: MAY PLAY A ROLE IN PLANT DEFENSE. HAS PROBABLY NO CXALATE OXIDASE ACTIVITY EVEN IF THE ACTIVE SITE IS CONSERVED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structural analysis of Arabidopsis thaliana chromosome 5. IV. Sequence features of the regions of 1,456,315 bp covered by nineteen physically assigned Pl and TAC clones."; DNA Res. 5:41-54(1998).
                                               FUNCTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VSVG-CFVGFDASEPDSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: OLIGOMER (BELIEVED HEXAMER) (BY SIMILARITY).
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2002 (Rel. 41
n synthetase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222
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                                                                                                                                                                                                                                                                                                                                                                                                                                     28, Created)
28, Last sequence update)
41, Last annotation update)
use (EC 6.3.2.-) (HTS).
/ SB111;
PubMed=10671527;
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MANGANESE (BY SIMILARITY).

MANGANESE (BY SIMILARITY).

MANGANESE (BY SIMILARITY).

MANGANESE (BY SIMILARITY).

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                          Cochliobolus.
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Pred. No. 12;
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                                                                                                                               RESULT
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Best Local Similarity
""" Conser"
                                                                                                                   7_HPV32
                                 VE7_HPV32
P36827;
01-JUN-1994
01-JUN-1994
15-JUN-2002
E7 protein.
E7.
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BINDING
BINDING
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DOMAIN
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Interpro; IPR001242; Condensatn.
Interpro; IPR001280; Ppantne_attach.
Pfam; PF00501; AMP-binding; 4.
Pfam; PF00550; pp-binding; 4.
Pfam; PF00658; Condensation; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M98024; AAA33023.1; -. HSSP; P14687; 1AMU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entitles requires a license agreement (S or send an email to license@isb-sib.ch).
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           Human papillomavirus type 32 Viruses; dsDNA viruses, no R
                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00012; PHOSPHOPANTETHEINE; PROSITE; PS00455; AMP_BINDING; 3. PROSITE; PS50075; ACP_DOMAIN; 4.
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                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                      DOMAIN
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-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-3 IS THE INITIATOR.
Papillomavirus
                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00154; AMPBINDING
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                                                                                                                                                                                         5 GCFVGFDASEPDSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European Bioinformatics Institute. The by non-profit institutions as long ifted and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Non-ribosomal peptide synthetase, able to activate proline and AEO (2-amino-9,10-epoxi-8-oxodecanoic acid), and epimerize L-Pro. Catalyzes the production of HC-toxin: a cyclic tetrapeptide. Activates and thioesterifies L-Pro, and epimerizes it to D-Pro; also uses D-Ala as a substrate but this is epimeriz.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COFACTOR:
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                                                                                                                                                                  GCFVPLDPSYPHER
                                                                                                                                                                                                                                                                                                                                                                                                                         Multifunctional
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                                                       (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONTAINS 4 COVALENTLY BOUND PHOSPHOPANTETHEINES. NON-RIBOSOMAL BIOSYNTHESIS OF HC-TOXIN.
Y: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYN
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                                                                                                                                                                                                                                                                 574637
                                                                                                                                                                                                                                                                                                                                                                                                                        enzyme; Phosphopantetheine; Repeat.
            RNA
                                                                                                                                                                                                                                                                        DOMAIN 4.

ACYL CARRIER (ACP) 2.

ACYL CARRIER (ACP) 3.

ACYL CARRIER (ACP) 3.

ACYL CARRIER (ACP) 4.

PHOSPHOPANTETHEINE (BY SIMILARITY).

PHOSPHOPANTETHEINE (BY SIMILARITY).

PHOSPHOPANTETHEINE (BY SIMILARITY).

PHOSPHOPANTETHEINE (BY SIMILARITY).

PHOSPHOPANTETHEINE (BY SIMILARITY).
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Pred.
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           stage;
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                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                0331D9C5400163A5
                                                                                                         104
            Papillomaviridae;
                                                                                                                                                                                                             Db ...
3.6e+02;
6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no restrictions ong as its content is in
                                                                                                         ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Usage
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                                                                                                                                                                                                                                      Length 5217;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cyclic peptide
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01-NOV-1995 (Rel.
16-OCT-2001 (Rel.
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Pfam; PF00527; E7; 1.
Early protein; Transcription regulation; Oncogene;
                                                                                                                                                                                                   Proc.
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Voltage-dependent anion-selective channel protein 1 (VDAC-1)
Voltage-dependent anion-selective voltage-dependent anion channel
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P45879;
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                                                                                                                                                                                                                                              membranes.";
                                                                                                                                                                                                                                                                   constitutes a large-conductance anion channel in
                                                                                                                                                                                                                                                                                                                           Siemen D.;
                                                                                                                                                                                                                                                                                                                                            Kremer M.,
                                                                                                                                                                                                                                                                                                                                               Dermietzel R., Hwang
Kremer M., Deutzmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
Bovidae; Bovinae; Bo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
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                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94119914;
                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Primer-directed sequencing of human papillomavirus types.";
Curr. Top. Microbiol. Immunol. 186:13-31(1994).
                                                                                                                                                                                                                                                                                                 'Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BR1-VDAC).
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                                                                                                                  C. Natl. Acad. Sci. U.S.A. 91:499-503(1994).

FUNCTION: FORMS A CHANNEL THROUGH THE MITOCHONDRIAL OUTER MEMBRANE AND ALSO THE PLASMA MEMBRANE. THE CHANNEL ALLOWS DIFFUSION OF SMALL HYDROPHILIC MOLECULES; IT ADOPTS AN OPEN CONFORMATION AT LOW OR ZERO MEMBRANE POTENTIAL AND A CLOSED CONFORMATION AT POTENTIALS
     TISSUE
                                                ABOVE 30-40 MV. THE OPEN STATE HAS A WEAK ANION SELECTIVITY WHEREAS THE CLOSED STATE IS CATION-SELECTIVE. SUBCELLULAR LOCATION: OUTER MEMBRANE OF MITOCHONDRIA AND PL
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     SPECIFICITY:
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                                                                                                                                                                                                                                                                                            localization
     PREDOMINANTLY IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB Pred. No. 9.8; 3; Mismatches
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Fishman G.I.,
                                                                                                                                                                                                                                                                                               brain-derived
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     BRAIN ASTROCYTES
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Best Local S
Matches 7
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Voltage dependent anion-selective channel protein
                                                                                              muse by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                 Pfam; PF01459;
                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-New
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                                                  [nterPro;
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PROSITE; PS00558; EUKARYOTIC_PORIN;
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-1- SIMILARITY: BELONGS TO THE EUKARYOTIC MITOCHONDRIAL PORIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 INLGCDVDFDIAGPSIR 138
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DOMAIN: CONSISTS MAINLY OF MEMBRANE-SPANNING SIDED BETA-SHEETS.

SIMILARITY: BELONGS TO THE EUKARYOTIC MITOCHONDRIAL PORIN FAMILY.
                                                                                                                                                            European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                       NITTED (DEC-1999) to the EMBL/GENBANK/DDBJ databases.
FUNCTION: FORMS A CHANNEL THROUGH THE MITTOCHONDRIAL OUTER MEMBRANE AND ALSO THE PLASMA MEMBRANE. THE CHANNEL ALLOWS DIFFUSION OF SMALL HYDROPHILIC MOLECULES; IT ADOPTS AN OPEN CONFORMATION AT LOW.
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                                                                                                                                                                                                                                                             MEMBRANE (BY SIMILARITY).
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                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through
sen the Swiss Institute of Bioinformatics and the EN
                                             AF209725; AAF22835.1; -. Pro; IPR001925; Porin_Euk.
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 ; PR00185;
E; PS00558;
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                               Euk_porin;
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                  EUKARYTPORIN.
EUKARYOTIC_PORIN;
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41.2%;
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Pred. No.
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27;
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                                                                                                                                                                              outstation
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                                                                                                                              commercia.
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RESULT
POR1_MO
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Best Local Similarity
Thes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ъ
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MOD_RES
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _MOUSE
   MGD; MGI:106919; Vdac1
                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resta
                                                                                                                                                                                            -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; PL-VDAC1 (SHOWN HERE) AND MT-VDAC1; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: HIGH LEVELS OF EXPRESSION DETECTED IN HEART,
KIDNEY, BRAIN, AND SKELETAL MUSCLE. NOT EXPRESSED IN TESTIS.
-!- DOMAIN: CONSISTS MAINLY OF MEMBRANE-SPANNING SIDED BETA-SHEETS.
-!- SIMILARITY: BELONGS TO THE EUKARYOTIC MITOCHONDRIAL PORIN FAMILY.
                                            EMBL; U30840;
                                                                          or send
                                                                                                     use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDAC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Voltage-dependent anion-selective channel protein 1 (VDAC-1) (mVDAC1)
(mVDAC5) (Outer mitochondrial membrane protein porin 1) (Plasmalemmal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q60932;
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                           anion channel isoform."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buettner R., Papoutsoglou G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION, AND ALTERNATIVE SPLICING MEDLINE=20202612; PubMed=10716730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     voltage-dependent anion channel isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Outer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomics 33:283-288(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Isolation, characterization, and mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sampson M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96301405; PubMed=8660977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM MT-VDAC1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POR1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Evidence for secretory pathway localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 INLGCDVDFDIAGPSIR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VSVGCFVGFDASEPDSR 18
                                                                                                                                                                                                                                                                                                      ABOVE 30-40 MV. THE OPEN STATE HAS A WEAK ANION SELECTIVITY WHEREAS THE CLOSED STATE IS CATION-SELECTIVE. SUBCELLULAR LOCAFION: MITOCHONDRIAL VDAC1 (MT-VDAC1) IN OUTER MEMBRANE OF MITOCHONDRIA AND PLASMALEMMAL VDAC1 (PL-VDAC1) IN
                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: FORMS A CHANNEL THROUGH THE MITOCHONDRIAL OUTER MEMBRANE AND ALSO THE PLASMA MEMBRANE. THE CHANNEL ALLOWS DIFFUSION OF SMALL HYDROPHILIC MOLECULES; IT ADOPTS AN OPEN CONFORMATION AT LOW OR ZERO MEMBRANE POTENTIAL AND A CLOSED CONFORMATION AT POTENTIALS
                                                                                                                                                                                                                                                                                           PLASMA MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OR VDAC5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           membrane;
                                                                          an
                                                                        requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282 AA;
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                                             AAB47777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=10716730;
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Rodentia;
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30609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craigen W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB
Pred. No. 27;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scemes E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  97:3201-3206(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spray D.C., Dermietzer n.,
Tion of a voltage-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of two mouse mitochondrial
                                                                                                                      as its content
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                                                                                                     Usage
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                                                                                                                                   restrictions
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Best Local
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Best Local
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MOD_RES
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGK_PARPR
000869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARSPLIC
SEQUENCE
KYNU_HUMAN
Q16719;
                                                                                                                                                                                                                                                                                                                            NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1902 (Rel. 41, Last annotation update)
Phosphoglycerate kinase (EC 2.7.2.3) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00558; EUKARYOTIC_PORIN; 1.
Outer membrane; Porin; Mitochondrion; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  Transferase; Kinase; Glycolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF001849; AAB58241.1; -. HSSP; P00560; 1QPG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Paramecium
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                                                                                                                                259
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                                                                                                                              PTDFVCGTGLDASSPVALH 277
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                                                                                                                                                                                                                                                                                                                                                                                         PF00162; PGK; 1.
TE; PS00111; PGLYCERATE_KINASE; PARTIAL.
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7; Conserv
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367 /
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86
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                      STANDARD;
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86
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DICYCLOHEXYLCARBODINHIDE (BY SIMILARITY).
MISSING (IN ISOFORM MT-VDAC1).
; C0710C1717063B32 CRC64;
                                                                                                                                                                                                                                                        Score 40;
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                                                                                                                                                                                                                                        Pred. No. 36;
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                                                                                                                                                                                                                                                          DB 1; Length 367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KYNU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Kynureninase (EC 3.7.1.3) (L-kynurenine hydrolase).
                                                                                                                 Hydrolase; Pyridoxal phosphate; Acetylation.

MOD_RES 1 1 ACETYLATION (BY SIMILARITY).

BINDING 276 276 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extremental Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- CATALYTIC ACTIVITY: L-3-hydroxykynurenine + hydroxyanthranilate + L-alanine.
-i- COFACTOR: PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Hepatoma;
MEDLINE=96314506; PubMed=8706755;
                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                       Genew;
                                                                                                                                                                                                                                                                         EMBL; U57721;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alberati-Giani
                                                                                                                                                                                                                                                                                                                                                                        modified and this statement
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SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYDROXYANTHRANILIC ACIDS (3-OHAA), RESPECTIVELY. HAS A PREFERENCE FOR THE L-3-HYDROXY FORM. ALSO HAS CYSTEINE-CONJUGATE-BETA-LYASE ACTIVITY (BY SIMILARITY).

CATALYTIC ACTIVITY: L-Kynurenine + H(2)O = anthranilate + L-alanine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFLAMMATORY CONDITIONS.
SIMILARITY: BELONGS TO THE KYNURENINASE FAMILY. SLIGHTLY RELATO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES TESTED (HEART, PLACENTA, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY AND PANCREAS, HIGHEST LEVELS FOUND IN PLACENTA, LIVER AND LUNG. EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: CATALYZES THE CLEAVAGE OF L-KYNURENINE (L-KYN) HYDROXYKYNURENINE (L-30HKYN) INTO ANTHRANILIC (AA) AND 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDUCTION: INCREASED LEVELS IN SEVERAL CEREBRAL
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C., Lahm H.-W.,
                                                                                                 276
465 F
  Conservative
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                                                                                                    52351 MW;
                         38.1%;
85.7%;
μ<u>α</u>
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                            Pred. No.
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Mismatches
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01-AUG-1992
15-JUN-2002
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Pfam; PF00273; transport_prot; 3.
PRINTS; PR00802; SERUMALBUMIN.
                                                                                                                                                    EMBL; X60688; CAA43098.1;
EMBL; V00381; CAA23680.1;
PIR; S15571; ABCHS.
HSSP; P02768; 1E7B.
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use
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Hache R.J.G., Wiskocil R., Vasa M., Roy R.N., Lau P.C.K., Deeley R.G. "The 5' noncoding and flanking regions of the avian very low density apolipoprotein II and serum albumin genes. Homologies with the egg
                                                                                Plasma;
                                                                                           PROSITE;
                                                                                                    SMART;
                                                                                                             ProDom; PD002486;
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Biochem. Biophys.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol.
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                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: PLASMA.
SIMILARITY: BELONGS TO THE ALB/AFP/VDB:
SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
                                                                                                                                                                                                                                                                                                                           BINDING CAPACITY FOR WATER, CA++, NA+, BILIRUBIN AND DRUGS. ITS MAIN FUNCTION COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
                                                                                                                                                                                                                                                                                                                                                            FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        protein genes.";
ol. Chem. 258:4556-4564(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     albumin
                                                                                                  SM00103; ALBUMIN;
                                                                                                                                                                                                     non-profit institutions as long as its content is in no way d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                               Metal-binding;
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(Rel. 23,
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Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                  hys. Res. Commun. 78:1060-1066(1977).
SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD APACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     precursor
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EMBL/GenBank/DDBJ databases.
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COPPER (
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; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                   biogenesis and encodes a peroxisomal matrix protein with be carboxy and amino-terminal targeting signals.";
J. Cell Biol. 127:737-749(1994).
-i- FUNCTION: ESSENTIAL FOR PEROXISOME BIOGENESIS. MAY PLAY TRIGGERING THE PROTEIN IMPERCY COMPETENCE OF INDIVIDUAL PEROXISOMES. IT MAY INTERACT WITH PERB (PEX10).
-i- SUBCELLULAR LOCATION: Peroxisomal; matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pichia angusta (Yeast) (Hansenula polymorpha).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Pichia.
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95050945; PubMed=Waterham H.R., Titorenko
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
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NCBI_TaxID=4905;
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                                                                                                                                                                                                                            the European
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PEROXISOMAL MATRIX PROTEIN PERI
MICROBODY TARGETING SIGNAL (POT:
A9AC534204F50C7D CRC64;
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Sp_barcheri
Sp_human:*

Sp_invert
6: sp_invert
6: sp_mamma
7: sp_mhc:*
8: sp_mamma
9: sp_pha*
10: sp_p)
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12: sp_r
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1 PVSVGCFVGFDAS
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               Q9zt62 cucumis sati
Q8vwn6 pisum sativ
Q9m4m7 persea amer
Q8u687 agrobacteri
Q9fz85 arabidopsis
Q8uf84 agrobacteri
Q9fnd9 arabidopsis
Q8uf84 agrobacteri
Q9fnd9 arabidopsis
Q8uf84 brucella me
Q8vea8 mus musculu
Q9yhd2 gallus gall
Q9yhd2 gallus gall
Q9yvwg rattus sp.
Q49942 mycobacteri
Q9vvq2 drosophila
Q91254 arabidopsis
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     arabidopsis
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O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 Q8VWN6
Q8VWN6;
01-MAR-2002
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF073744; AAD02832.1; -
Glycosyltransferase; Transferase.
SEQUENCE 784 AA; 86920 MW; 3B06A491F0908933 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-LEAF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3659;
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                                                                                                                                                                                       1 PVSVGCFVGFDASEPDSRH 19
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Q9LCH6
Q08410
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Q9XUS4
Q9M8Z4
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Q51720
Q9XW86
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Q8R0F7
Q92P85
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Q9MCH9
Q9U249
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09av10 oryza sativ
0942t6 oryza sativ
0971e6 sulfolobus
0971e6 sulfolobus
0971e6 sulfolobus
0971e6 sureptococc
09u249 caenorhabdi
09xeq8 sorghum bic
094ay8 arabidopsis
09gzfl caenorhabdi
08r0f7 mus musculu
092p85 rhizobium m
023053 arabidopsis
09cxf0 mus musculu
031813 bacillus su
09yb34 aeropyrum p
09kbf5 bacillus su
09yb34 aeropyrum
09kbf5 bacillus su
09yb34 aeropyrum
09kbf5 bacillus su
09gm66 caenorhabdi
09fvh5 prunus arme
09lch6 streptomyce
008410 shewanella
08u1g8 pyrococcus
05z785 acinetobact
09xus4 caenorhabdi
09m8z4 arabidopsis
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Gaps

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RESULT
Q8U687
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DT 01
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01-JUN-2002 (TrEMBLrel. 21, Las
01-JUN-2002 (TrEMBLrel. 21, Las
Hypothetical protein Atu6048.
ATU6048 OR AGR_PTI_100.
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Spermatophyta; Magnoliophyta;
eurosids I; Fabales: Pahara
           Bacteria;
                                                                                                         Q8U687;
                                                                                                                                                                                                                                                                           cold storage of avocado (Persea americana Mill Submitted (MAR-1999) to the EMBL/GenBank/DDBJ EMBL; AJ133148; CAB77245-1; -
SEQUENCE 779 AA; 85368 MW; C3A8B4316031678
                                                                                                                                                                                                                                                                                                                                 STRAIN=CV. HASS; TISSUE=MES Zamorano J.P., Evans A.D., Merodio C., Grierson D.;
                                                                                                                                                                                                                                                                                                                                                                                                      Persea americana (Avocado).
Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Laurales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel 15, O1-OCT-2000 (TrEMBLrel 19, O1-DEC-2001 (TrEMBLrel 19, Putative seed imbibition pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9M4M7;
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STRAIN-CV. WUNDER VON KELVEDON; TISSUE-SEED;
STRAIN-CV. WUNDER VON KELVEDON; TISSUE-SEED;
Peterbauer T., Mach L., Mucha J., Richter A.;
Peterbauer T., Mach L., Mucha J., Richter A.;
"Molecular characterization of raffinose synthase from pea sativum L.) seeds.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ426475; CADZ0127.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Raffinose
RFS.
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                                                                                                                                                                                                                                                                                                "Isolation and characterization of cDNAs for mRNAs regulated cold storage of avocado (Persea americana Mill.) fruit."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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NCBI_TaxID=3888;
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            Proteobacteria;
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798 AA; 88717 MW; 81
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protein.
            alpha
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            subdivision;
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No.
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                                  ATCC 33970).
                                                                                                                                                                                                                                        DB 10;
9.7;
                                                                                                                                                                                                                                                                                                                                                                                                          Lauraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                    Embryophyta;
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            Rhizobiaceae
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RESULT
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                         SEQUENCE FROM N.A.
Yamada K., Banh J., C
Lee J.M., Onodera C.S
Yamamura Y., Yu G., Y
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Q9FZ85;
Q1-MAR-2001
Q1-MAR-2001
Q1-JUN-2002
                                                                                                                                                         SEQUENCE FROM N.A. Palm C.J., Conway A.B., Conn L., Hansen N.F., Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks Buehler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A., Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M., Liu S., Mukharsky N., Pham P., Sakano H., Shir Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis F Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V. K., Zhou Y., Chen L., Wood G.E., Almelda N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D. Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W.;
"The genome of the natural genetic engineer Agrobacterium tumefacien"
                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphatase).
F26II6.2 OR ATIG18640.
F26II6.2 OR ATIG18640.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE00943; AA1462841; -.
EMBL; AE007931; AAK91006.1; -.
Hypothetical protein; Plasmid;
SEQUENCE 836 AA; 91964 MW;
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  Yamamura Y., Yu
Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3-phosphoserine phosphatase
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Chang C.H., Chang E., Dale J.M.,
S. Quach H.L., Tang C., Toriumi
Yu.S., Bowser L., Carninci P., Cr
ida J., Jones T., Kamiya A., Karli
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3C61FD8318D39DF1 CRC64;
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                              Chen H
                           M., Wu H.C.,
hen H., Cheuk R.,
                                                                                Goldsmith A.D.,
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Markelz
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wis R.W.
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RESULT
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                                                  OBUF84 PRELIMINAKY;

OBUF84;

O1-JUN-2002 (TrEMBLrel. 21, Created)

O1-JUN-2002 (TrEMBLrel. 21, Last sequence

O1-JUN-2002 (TrEMBLrel. 21, Last annotati

E Hypothetical protein Atul515

N ATUL515 OR AGR.C_2794.

N AGROBACTERIAN TUMEFACIENS (Strain C58 / Spantaria: Proteobacteria; alpha subdivis
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01-NOV-1998
01-NOV-1998
01-JUN-2002
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Ho C., No
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Interpro; IPR004469; SerB.
Pfam; PF00702; Hydrolase; 1.
TIGRFAMS; TIGR00338; SerB; 1.
SEQUENCE 295 AA; 32318 MW; F14C95E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning and characterization of PSP.";
"Molecular cloning and characterization of PSP.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ dat
EMBL; AB018409; BAA33807.1;
EMBL; AB018408; BAA33806.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Full Length cDNA of gene At1g18640 (GI:15221827)."; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databa EMBL; AC026238; AAF98410.1; -
EMBL; AY065351; AAL38792.1; -
NCBI_TaxID=176299; [1]
                                           Rhizobiaceae;
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SEQUENCE 295 AA; 32302 MW;
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InterPro; IPR004469; SerB.
Pfam; PF00702; Hydrolase; 1.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Narusaka M.,
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M., Nguyen M., I
Southwick A., !
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Palm C.J., Sakurai T., Sa
Shinozaki K., Davis R.W.,
                                                                                                                                                  Created)
Last sequence update)
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Pred. No.
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                                                                  subdivision;
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                                                             ATCC 33970).
sion; Rhizobiaceae
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W., Ecker J.
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Matches 8
SEQUENCE FROM N.A.
Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Ecker J., Theologis A., Davis R.W.;
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MEDILINE-21608550; PubMed-11743193;

WOOD D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Almeida N.F. Jr., Woo L.

Chen Y., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,

Kordon C., Rouse G., Saenphimmachak C., W.Z., Romero P., Gordon

Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry

Gordon Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan

Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                              "Structural analysis of Arabidops
Sequence features of the regions
physically assigned Pl clones.";
DNA Res. 4:291-300(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., W. Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Mar Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub
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                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo; Spermatophyta; Magnoliophyta; eudlcotyledons; core eudlcots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Science 294:2323-2328(2001
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"Genome sequence of the plant pathogen "Genome sequence of the plant pathogen";
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8; Conserv
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36937 MW; C06405E207BF643A CRC64;
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47.18;
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RESULT 10
Q8VEA8
ID Q8VEA
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Q8YFH2
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Best Local Similarity
Matches 10; Conserv
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Best Local
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 Q8VEA8;
Q8VEA8;
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Sakurai T., Theologis A., Davis R.W.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AB06770; BAB11595.1; -EMBL; AN062781; AAA12859.1; -EMBL; AY081645; AAM10207.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8YFH2;
Q8YFH2;
                                                                                                                                                                                                                                                                         STRAIN=16M / ATCC 23456 / BIOTYPE 1;

MEDLINE=20020109; PubMed=11756688;

MEDLINE=20020109; PubMed=11756688;

DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.

IVanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,

Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.

Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,

Haselkorn R., Kyrpides N., Overbeek R.;
                                                                                                                                                                       InterPro; IPR005289; GTP-bindding_dom.
InterPro; IPR002917; MMR_HSR1.
InterPro; IPR005225; Small_GTP.
Pfam; PP01926; MMR_HSR1; 1.
TIGRFAMS; TIGR00650; MG442; 2.
TIGRFAMS; TIGR00231; small_GTP; 2.
                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002). EMBL; AE009590; AAL52731.1; -.
                                                                                                                                                                                                                                                       "The genome sequence of the facultative intracellular pathogen Brucella melitensis.";
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Bacteria; Proteobacteria;
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RESULT 11
Q9YHD2
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Matches 7
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Best Local :
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Q9YHD2;
Q1-MAY-1999
Q1-MAY-1999
Q1-JUN-2002
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SEQUENCE
                                                                                                                                               InterPro; IPR003878; SPRY_domain.
InterPro; IPR003877; SPRY_receptor.
Pfam; PF00622; SPRY; 1.
SMART; SM00449; SPRY; 1.
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                                                                                                                                                                                                              Submitted (OCT-1998) to the EMBL/GenBank/DDBJ EMBL; aF098788; aAC69888.1; -.
                                                                                                                                                                                                                                                                                        TISSUE=BRAIN;
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PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1
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PRINTS; PR00449; RASTRNSFRMNG
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Interpro; IPR001806; Ras_trnsfrmng
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                                                                                                                                                                                                                                                    "Identification of ChURP,
                                                                                                                                                                                                                                                       Lodge A.P., Walsh A., McNamee C.J., "Identification of ChURP, a Nuclear
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                                                        7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
                                                                                                                      757
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 10, (TrEMBLrel. 10, (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                    AA;
354
                             16
                                                                                                                                                                                                                                                                                                                                                               ; Chordata; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; (Rodentia; S
                                                                                                                      84179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22502 MW;
                                                                          42.9%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.9%;
46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20, Last sequence update)
21, Last annotation updat
                                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                                                                                                         protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last annotation update)
                                                                          Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
;; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33353842079CF6FC CRC64;
                                                                                                                      7FA04ED9E1776D1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                          Mismatches
                                                                                                                                                                                                                                                        Moss D.J.;
Calmodulin-Binding Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    757
                                                                           64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                      DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AΑ
                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                              databases
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                                                                                      Length 757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 199;
                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                          0;
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                                                                                                                                                                                                                                                          Related
                                                           Gaps
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                                                          0;
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PRELIMINARY;

PRT;

202

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Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q49942 PRELIMINARY; PRT; 3
Q49942;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seque)
01-MAR-2002 (TrEMBLrel. 20, Last annot Hypothetical protein MI2346.
MI2346 OR L518_F3_81 OR MICB2407.04.
Mycobacterium leprae.
                                                                                                                                                                                                                                                          MEDLINE-1128732; PubMed-11234002;

Gole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,

Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,

Wheeler R., Basham D., Brown D., Chillingworth T., Connor R.,

Mungall K., Basham D., Brown D., Chillingworth T., Fraser A., Hamlin N.,

Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,

Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,

Murphy L., Oliver K., Quall M.A., Rajandream M.A., Rutherford K.M.,

Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,

Rutter S., Seeger K., Simon S., Simmonds M., Skelton J.R.,

Rutter S., Seeyens K., Taylor K., Whitehead S., Woodward J.R.,
                  Smith D.R., Robison K.;
Submitted (MAY-1998) to the
EMBL; AL583925; CAC31862.1;
EMBL; U00023; AAA17366.1; -
EMBL; AL023596; CAA19144.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS0011; PROTEIN KINASE_ATP;
ATP-h1-A1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 01-MAY-2000 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                    "Massive gene decay in the leprosy Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                       Squares S., S
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinomycetales;
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00069; pkinase; ProDom; PD000001; Euk_p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yazaki N., Hosoi Y., Kawabata K.,
Ohta M., Kawasaki T., Itoh N.;
"Differential expression patterns
fibroblast growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94293355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fibroblast growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP-binding; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      brain."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P11362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000719; Euk_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 PLGEGCFGQVVRAEALGMDSSRPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 PVSVGCF-----VGFDASEPD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neurosci. Res.
AL023596;
ma; ML2346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
9; Conser
                                                                                                                                                 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterineae;
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; 21986 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37:445-452(1994).
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.9%;
37.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13, Created,
13, Last sequence update)
21, Last annotation update)
... receptor 4, FGFR-4 (Fragment).
                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 24;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8F87690566EBFA31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miyake A., Minami M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of mRNAs for members of the
                                                                                                                                                                                                                            bacillus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGFR-1-FGFR-4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Length 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Satoh
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RESULT 14
Q9VVQ2
ID Q9VVQ
AC Q9VVC
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                      Adams M.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Sutton G.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RS Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RS Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklog G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklog G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Brokstein P., Brottier P.,
RA Borkva D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtls K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Borkva D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkva D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Dutbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Harris M.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mcherson D.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Sanders R.D.C., Scheeler F., Shen H.,
RA Shie B., C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shie B., Shang R., Wei M., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Q9VVQ2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 01-MAY-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Complete proteome. SEQUENCE 301 AA; 33939 MW; CF11EF2EEAE7AOAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pterygota; Neoptera; Endopte
Ephydroidea; Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit : Eukaryota; Metazoa; Arthropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20196006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200
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les 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein.
                FBgn0036791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213
47361 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.9%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endopterygota; Diptera; Brachycera; Muscomorpha;
ilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13,
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F0519C00EFAA569C CRC64;
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Score

44;

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RESULT OPLESTATION OF THE PROPERTY OF THE PROP
Search completed: March 27, Job time: 13.6585 secs
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,

Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;

Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

[2]
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

BU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AL162971; CAB85985.1; -.

InterPro; IPR000268; Hsp20.

InterPro; IPR000334; Zn_carbOpept.

PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.

PROSITE; PS01031; HSP20; 1.

Hypothetical proteai.

Hypothetical proteai.

Hypothetical proteai.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O9LZ54 PRELIMINARY; PRT; 498 AA.
09LZ54; O1-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 55.5 kDa protein.
T22P11_70
                                                                                                                                           5 GCFVGFDASE 14
||| ||| |:
132 GCFTGFDKSD 141
                                                                                                                                                                                                                                                                                    Local Similarity 70.0 hes 7; Conservative
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70.0%;
                                        2003, 10:05:59
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Pred. No. 61;
1; Mismatches 2; Indels
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2; Mismatches
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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     of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/U
2: /cgn2_6/ptodata/2/pubpaa/U
3: /cgn2_6/ptodata/2/pubpaa/U
4: /cgn2_6/ptodata/2/pubpaa/U
5: /cgn2_6/ptodata/2/pubpaa/U
6: /cgn2_6/ptodata/2/pubpaa/U
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9: /cgn2_6/ptodata/2/pubpaa/U
11: /cgn2_6/ptodata/2/pubpaa/U
12: /cgn2_6/ptodata/2/pubpaa/U
13: /cgn2_6/ptodata/2/pubpaa/U
14: /cgn2_6/ptodata/2/pubpaa/U
15: /cgn2_6/ptodata/2/pubpaa/U
16: /cgn2_6/ptodata/2/pubpaa/U
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19: /cgn2_6/ptodata/2/pubpaa/U
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12: /cgn2_6/ptodata/2/pubpaa/U
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14: /cgn2_6/ptodata/2/pubpaa/U
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105
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Match Length
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     /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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1: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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     DB
     10 US-09-873-880-34

10 US-09-873-880-36

3 US-09-738-6256-4094

10 US-09-924-256A-34

10 US-09-924-256A-34

10 US-09-924-256A-34

10 US-10-081-806-6

10 US-10-081-806-6

10 US-09-940-244-6

10 US-09-940-244-259

10 US-09-777-430A-8

10 US-09-777-430A-15

10 US-09-777-430A-15

10 US-09-777-430A-20

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10 US-09-777-430A-23

10 US-09-813-153-110
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                               Sequence 6, Appli
Sequence 259, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 21, Appli
Sequence 20, Appli
Sequence 23, Appli
Sequence 26, Appli
                                                                                                                                                                                                                                                                                                                                        Description
   Sequence
Sequence
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Sequence 36, Appl
Sequence 4094, Ap
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Sequence 34, Appl
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37	37	37	37.5	37.5	37.5	37.5	37.5	37.5	37.5	37.5	38	38	38	38	38	38	38	38	38	38	38	39	39	39	39
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US-09-738-626-3981	US-09-864-761-48087	US-09-975-036-6	US-10-131-685-20	US-10-128-870-20	US-09-810-796-14	US-09-813-148-4	US-10-131-685-23	US-10-128-870-23	US-09-738-626-3975	US-09-891-139A-12	US-09-940-925A-5	US-09-940-244-5	US-10-074-328-5	US-10-081-806-5	US-10-033-297-5	US-09-894-998-12	US-09-738-626-6376	US-09-838-955-3	US-09-853-450-20	US-09-791-279-188	US-09-894-998-11	US-09-940-925A-8	US-09-940-244-8	US-10-074-328-8	US-10-081-806-8
Sequence 3981, Ap	Sequence 48087, A	Sequence 6, Appli	Sequence 20, Appl	Sequence 20, Appl	Sequence 14, Appl	Sequence 4, Appli		Sequence 23, Appl	Sequence 3975, Ap	12,	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	>	Sequence 12, Appl	0	Sequence 3, Appli	Sequence 20, Appl	Sequence 188, App	Sequence 11, Appl	•	•	Sequence 8, Appli	Sequence 8, Appli

ALIGNMENTS

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APPLICANT: Sewalt, Vincent
APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Allen, Stephen M.
TITLE OF INVENTION: GLYCINE METABOLISM ENZYMES
FILE REFERENCE: BB1192 US CIP
CURRENT APPLICATION NUMBER: US/09/873,880
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/363,321
PRIOR APPLICATION NUMBER: 09/363,321
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: 60/094,839
PRIOR APPLICATION NUMBER: 00/964,839
PRIOR FILING DATE: July 31, 1998
                                                                                                   RESULT 2
US-09-873-880-36
US-09-873-880-36
Sequence 36, Application US/09873880
Patent No. US20020123118A1
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                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Thehes 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT; CRGANISM: Zea mays; US-09-873-880-34
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                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Microsoft Office 97
SEQ ID NO 34
APPLICANT: Sewalt, Vincent
APPLICANT: Falco, S. Carl
APPLICANT: Allen, Stephen M.
APPLICANT: Allen, Stephen M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 42
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209 TLGEYAGFDPTEPTSR 224
                                                                                                                                                                                                                                                                        3 SVGCFVGFDASEPDSR 18 ::| : | | | | | |
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Pred. No. 12;
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RESULT 4
US-09-924-256A-22
: Sequence 22, Application US/09924256A
: Patent No. US20020127659A1
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; LENGTH: 382
; TYPE: PRT
; ORCANISM: Corynebacterium glutamicum
US-09-738-626-4094
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US-09-738-626-4094
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GENERAL INFORMATION:
APPLICANT: Waters, Barba
APPLICANT: Miao, Vivian
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APPLICANT:
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Matches 9; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/363,321
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: 60/094,839
PRIOR FILING DATE: July 31, 1998
NUMBER OF SEQ ID NOS: 42
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CURRENT APPLICATION NUMBER: US/09/873,880
CURRENT FILING DATE: 2001-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                           2 VSVGCFVGFDASEP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 GCFVGFDASEPDSR 18
                                                                                                                                                            VTVGLFVVLDASSP 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKEDA, MASATO
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HARUHIKO
                                                                                                                                                                                                                                                40.0%;
64.3%;
                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
24;
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                                                                                                                                                                                                                                                                 Length 382;
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                                                                                                                                                                                                                                0;
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; SEQ ID NO 34
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Leptogium corniculatum
US-09-924-256A-34
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; LOCATION: (136)
; OTHER INFORMATION: Xaa-unknown amino acid
US-09-924-256A-22
                                                                                                                                              US-10-033-297-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-924-256A-34; Sequence 34, Apr
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LENGTH: 212
TYPE: PRT
                                                                                                          Sequence 6, Application US/10033297 Publication No. US20020187486A1
                                                                                                                                                                                                                                                                                          Best Local Similarity Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/924,256A CURRENT FILING DATE: 2001-08-08 PRIOR APPLICATION NUMBER: 08/861,774 PRIOR FILING DATE: 2001-04-13 NUMBER OF SEQ ID NOS: 94 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tong, Seow
TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR
TITLE OF INVENTION: BIOACTIVE MOLECULES
FILE REFERENCE: 9993-006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Waters, Barbara APPLICANT: Miao, Vivian APPLICANT: Ho, Yap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 08/861,774
PRIOR FILING DATE: 2001-04-13
NUMBER OF SEQ ID NOS: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/924,256A CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: TONG, SEOW
TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES
TITLE OF INVENTION: BIOACTIVE MOLECULES
FILE REFERENCE: 9993-006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Xanthoparmelia cumberlandia FEATURE:
                                                                                                                                                                                                                     22 PEDVGCYIGACATDYD 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 PEDVGCYIGACATDYD 37
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les 7; Conserv
                                                                                                                                                                                                                                                         1 PVSVGCFVGFDASEPD 16
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     TITLE OF
                                                                         APPLICANT: Hall,
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                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
Mast, Andrea L.
Brow, Mary Ann D.
INVENTION: Detection Of Nucleic Acids
                                                      Hall, Jeff G.
Lyamichev, Victor
                                                                                                                                                                                                                                                                                                             39.0%;
43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.0%;
                                                                                                                                                                                                                                                                                                             Score 41;
Pred. No.
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1; Mismatches
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36;
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                                                                                                                                                                                                                                                                                          0;
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STREET: 220 Montgomery Street, Suite 2200

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                                                                                                                                               Sequence 6, Application US/10081806 Publication No. US20020197623A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                 64 FVVFDAKAPSFRH 76
                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                      7 FVGFDASEPDSRH 19
                                  Hall, Jeff G.
Lyamichev, Victor I.
TITLE OF INVENTION: Invasive Cleavge Of Nucleic
NUMBER OF SEQUENCES: 69
CORRESPONDENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                              CORRESPONDENCE
                                                                                                                              APPLICANT: Prudent, James R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                            38.1%;
Similarity 61.5%;
8; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/823,516
FILING DATE: 24-MAR-1997
APPLICATION NUMBER: PCT/US97/01072
FILING DATE: 21-JAN-1997
APPLICATION NUMBER: US 08/759,038
FILING DATE: 02-DEC-1996
APPLICATION NUMBER: US 08/758,314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/033,297
FILING DATE: 12-No. US20020187486A1-2001
CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 12-JUL-1996
APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 02-DEC-1996
APPLICATION NUMBER: US 08/756,386
FILING DATE: 29-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 834 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             United States Of America
ADDRESS:
: Medlen & Carroll, LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequential Invasive Cleavages
                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 9;
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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US-10-074-328-6
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 FVVFDAKAPSFRH 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 FVGFDASEPDSRH 19
                                                                      ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FO)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/081,806
FILING DATE: 22-Feb-2002
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CURRENT APPLICATION DATA:
                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
                                                                                                                                                                                                                                                                   TITLE OF INVENTION: DETECTION OF NUCLEIC ACID INVADER-DIRECTED CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BROW, MARY ANN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 61.5
8; Conservative
            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/10074328
                                                                                                                                                                       STREET: 220 MONTGOMERY CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: California COUNTRY: United States Of America
                                                                                                                                                    STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/756,386
FILING DATE: CUNKNOWN
APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/599,491 FILING DATE: 24-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 834 amino acids
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                                                                                                                                                                                                                                                                                                       LYAMICHEV, VICTOR OLIVE, DAVID M. PRUDENT, JAMES R.
                                                                                                                                                                                                                                                                                                                                                                  GROTELUESCHEN HALL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.1%;
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Pred. No. 2
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                                                                                                                                                                                         STREET, SUITE 2200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9;
2.2e+02;
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NUMBER OF SEQ ID NOS: 422
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: B34
TYPE: PRT
ORGANISM: Thermus thermophilus
US-09-940-244-6
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                                                                                                                                                         US-09-940-925A-6
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                                                                                                 Sequence 6, Application US/09940925A Publication No. US20030054338A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09940244 Publication No. US20030044796A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          Query Match 38.1%;
Best Local Similarity 61.5%;
Matches 8; Conservative
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APPLICANT: Hall, Jeff G.
APPLICANT: Lyamichev, Victor
APPLICANT: Smith, Lloyd M.
TITLE OF INVENTION: Reactions on Dendrimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: FORS-06478
CURRENT APPLICATION NUMBER: US/09/940,244
CURRENT FILING DATE: 2002-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LEMGTH: 834 amino acids
                                                                                                                                                                                                                           64 FVVFDAKAPSFRH 76
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Local Similarity 61.5%;
nes 8; Conservation
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                           APPLICANT: BROW, MARY ANN D.

LYAMICHEV, VICTOR I.

OLIVE, DAVID M.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/599,491 FILING DATE: 23-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: INGOLIA, DIANE E. REGISTRATION NUMBER: P-40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/10/074,328 FILING DATE: 12-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: FORS-01802
SEQUENCES:
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Pred. No.
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Pred. No. 2.
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APPLICANT: Neri, Bruce P.
APPLICANT: Hall, Jeff G.
APPLICANT: Lyamichev, Victor
APPLICANT: Smith, Lloyd M.
TITLE OF INVENTION: Reactions on Dendrimers
FILE REFERENCE: FORS-06478
                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.1
SEQ ID NO 259
LENGTH: 836
                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Publication No.
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Best Local Similarity
Matches 8; Conserv
                                                                    Matches
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CURRENT FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 422
                                                                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                TYPE: PRT
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INFORMATION FOR SEQ ID NO: 6:
                                                                    Local Similarity
nes 8; Conserv
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                                 7 FVGFDASEPDSRH 19
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TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/940,925A
FILING DATE: 10-Jun-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
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ADDRESSEE: MEDLEN & CARROLL
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FVVFDAKAPSFRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 834 amino acids TYPE: amino acid
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TELEFAX: (415) 397-8338
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                                                                    Conservative
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 78
                                                                                     38.1%;
61.5%;
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61.5%;
                                                                   Score 40; DB 9; DP Pred. No. 2.2e+02; Signatches 5;
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Pred. No. 2.2e+02;
"'Cmatches 5;
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APPLICANT: Takova, Tsetska

APPLICANT: Neir, Bruce P.

TITLE OF INVENTION: Charge Tags and the Separation of Nucleic Acid Molecules

FILE REFERENCE: FORS-04912

CURRENT APPLICATION NUMBER: US/09/777,430A

CURRENT FILING DATE: 2001-02-06

NUMBER OF SEQ ID NOS: 85

SOFTWARE: PatentIn version 3.1

SEQ ID NO 8

LENGTH: 836

TYPE: PRT

ORGANISM: Thermus thermophilus

US-09-777-430A-8
                                                                                                                                                                                                                                                                                                             APPLICANT: Neil, Bruce P.
TITLE OF INVENTION: Charge Tags and the Separation of Nucleic Acid Molecules
FILE REFERENCE: FORS-04912
CURRENT APPLICATION NUMBER: US/09/777,430A
CURRENT FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 836
TYPE: PRT
ORGANISM: Thermus thermophilus
US-09-777-430A-11
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US-09-777-430A-8
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US-09-777-430A-11
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Sequence 15, Application US/09777430A
Patent No. US/20020128465A1
GENERAL INFORMATION:
APPLICANT: Lyamichev, Victor
APPLICANT: Skrzypczynski, Zbigniew
APPLICANT: Allawi, Hatim T.
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APPLICANT: Lyamichev, Victor
APPLICANT: Skrzypczynski, Zl
APPLICANT: Allawi, Hatim T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/09777430A Patent No. US20020128465A1 GENERAL INFORMATION:
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Allawi, Hatim T.
Wayland, Sarah R.
Takova, Tsetska
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61.5%;
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Pred. No. 2.2e+02;
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Pred. No. 2.2e+02;
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Search completed: March 27, Job time: 5.40244 secs
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US-09-777-430A-20
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                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 842
TYPE: PRT
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Best Local Similarity
Matches 8; Conserv
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SEQ ID NO 15
LENGTH: 842
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                                                                                                                                                Query Match
Best Local :
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APPLICANT:
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CURRENT FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 85
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APPLICANT: Takova, Tsetska
APPLICANT: Neir, Bruce P.
TITLE OF INVENTION: Charge Tags and the Separation of Nucleic Acid Molecules
FILE REFERENCE: FORS-04912
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Neir, Bruce P. TITLE OF INVENTION: Charge Tags and the Separation of Nucleic Acid Molecules FILE REFERENCE: FORS-04912
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lyamichev, Victor APPLICANT: Skrzypczynski, Z
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                                                                                                                             Local Similarity 61.9 es 8; Conservative
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Allawi, Hatim T.
Wayland, Sarah R.
Takova, Tsetska
Neir, Bruce P.
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Pred. No. 2.2e+02;
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Minimum
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Perfect score:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
         of hits satisfying chosen parameters:
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1: /cgn2_6/ptodata/1.

2: /cgn2_6/ptodata/1.

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length: 2000000000
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1 FGWCTWDAFYLTVI
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Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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     GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen Ltd.
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US-08-231-894A-11

US-08-231-894A-12

US-08-231-894A-13

US-08-231-894A-14

US-08-231-894A-14

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US-09-417-721-3

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US-08-946-234-5
US-08-100-744-4
US-08-284-784-4
US-08-854-811-4
PCT-US90-06962-1
US-07-830-330-1
US-08-187-780-3
                                    US-09-417-721-5

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US-08-439-725A-10	US-08-177-502-4	US-08-177-502-2	US-07-842-177A-1	US-08-023-757-4	US-08-023-757-2	US-07-959-369-7	US-07-959-369-6	PCT-US91-02186-6	US-08-325-186-1	US-08-438-439C-24	US-08-325-186-2	PCT-US95-09172-8	US-09-507-773-8	US-08-776-207-8	US-08-441-629-8	5314872-1	5175147-8
Sequence	 Sequence 	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Patent No.	Patent No.
10, Appl	4, Appli	2, Appli	1, Appli	4, Appli	2, Appli	7, Appli	6, Appli	6, Appli	~	24, Appl	2, Appli	8, Appli	•	8, Appli	8, Appli	. 5314872	. 5175147

ALIGNMENTS

γQ US-08-846-234-1 US-08-846-234-1 RESULT 1 Sequence 1, Application US/08846234 Patent No. 6166292 GENERAL INFORMATION: APPLICANT: OSUMI Chieko Query Match Best Local Similarity Matches 30; Conserv COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, VG CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/846,234 FILING DATE: ATTORNEY/AGENT INFORMATION: TELEPHONE: (703)-413-3 TELEFAX: (703)-413-222 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: CORRESPONDENCE ADDRESS: ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR APPLICANT: OSUMI Chieko APPLICANT: NOZAKI Jinshi APPLICANT: KIDA Takao TITLE OF INVENTION: RAFFINOSE SYNTHASE GENE, TITLE OF INVENTION: PRODUCING RAFFINOSE, AND MOLECULE TYPE: FRAGMENT TYPE: REGISTRATION NUMBER: 24,618 TELECOMMUNICATION INFORMATION: TELEPHONE: (703)-413-3000 NUMBER OF SEQUENCES: STREET: 1755 S. CITY: ARLINGTON STATE: VIRGINIA COUNTRY: USA ZIP: 22202 TOPOLOGY: TYPE: NAME: NORMAN F. OBLON LENGTH: FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC 30 amino acid 30 amino acids 100.0%; ilarity 100.0%; Conservative ((703)-413-2220 linear peptide internal 0; Score 181; DB 4; Pred. No. 5.2e-20; Mismatches Version #1.30 (EPO) METHOD FOR TRANSGENIC 0; Length Indels 30; PLANT 0, Gaps

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Patent No. 616629
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APPLICANT: MASCAR
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 784 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                         APPLICANT: OLSON, PAMELA
APPLICANT: OLSEN, DAVID
APPLICANT: CARRILLO, PEDRO A.
TITLE OF INVENTION: POLYPEPTIDE FUSIONS TO
TITLE OF INVENTION: INTERLEUKIN-1-LIKE POLY
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: NORMAN F. OBLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: OBLON, SPIVAK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: RAFFINOSE SYNTHASE GENE, METHOD FOR TITLE OF INVENTION: PRODUCING RAFFINOSE, AND TRANSGENIC NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: OSUMI Chiek
APPLICANT: NOZAKI Jins
APPLICANT: KIDA Takao
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                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: ami
TOPOLOGY:
                                                                 COUNTRY: USA
ZIP: 94304-1018
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CITY: Palo Alto
STATE: Californ
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GY: linear
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                                                                                                       California
                                                                                                                                      755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 181; DB 4; ilarity 100.0%; Pred. No. 2.7e-18; Conservative 0; Mismatches 0:
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ZHANG, SUNNY
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                                                                                                                                                          MORRISON & FOERSTER
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                                                              INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC:DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                              SEQUENCE CHARACTERISTICS:
                                                                                                        REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: PARK, FREDDIE K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: EXPRESSION OF FUSION POLYPEPTIDES
TITLE OF INVENTION: TRANSPORTED OUT OF THE CYTOPLASM WITHOUT LEADER SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                   TELLEFAX: (41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                              TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
FILING DATE: 02-AU
CLASSIFICATION: 43
                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/284,784
FILING DATE: 02-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                            STREET: 755 Page
CITY: Palo Alto
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                                                                                                                                                         NAME: PARK, FREDDIE K. REGISTRATION NUMBER: 3
                                                                                                                                                                                                       CLASSIFICATION:
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les 10; Conserv
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 STRANDEDNESS:
                              LENGTH:
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                amino acid
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                         132 amino acids
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VENTION: EXPRESSION OF FUSION POLYPEPTIDES
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OLSON, PAMELA S.
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PCT-US90-06962-1
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                                                                                                                                    Query Match
Best Local Similarity
Matches 10; Conserva
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                                                                                                                                                                                                                                                                                        TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284,784
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/100,744
FILING DATE: 02-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            NAME: Buffinger, Nicholas S
REGISTRATION NUMBER: 39,124
REFERENCE/DOCKET NUMBER: 220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON 6 FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: EXPRESSION OF FUSION POLYPEPTIDES
TITLE OF INVENTION: TRANSPORTED OUT OF THE CYTOPLASM WITHOUT LEADER
TITLE OF INVENTION: SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Olson, Pamela S. APPLICANT: Olsen, David R. APPLICANT: Cohen, Pedro A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 YCKNGGFFLRIHPDGRVDGVREKSD 34
                                                                                                                                                                                                                                     LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 12-MAY-1997 CLASSIFICATION: 435
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CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                                                                                                               TELEFAX:
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Local Similarity 40.0%;
                                                                                                  3 WCTWDAFYLTVHPQGVIEGVRHLVD 27
                                                                YCKNGGFFLRIHPDGRVDGVREKSD 34
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                                                                                                                                    Conservative
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                                                                                                                                                                                                                         linear
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                                                                                                                                                   33.18;
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                                                                                                                                 5; Mismatches
                                                                                                                                                   Score 60; DB 2; Length 132; Pred. No. 0.17;
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Pred. No. 0.
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US-07-830-330-1
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                                                                                                                                                                                                                                                                                                                                                                            Patent No. 5288704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 33.1%;
Best Local Similarity 40.0%;
Matches 10; Conservative
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                                                                                                                                                                                   APPLICANT: Mazue, Guy
TITLE OF INVENTION: SYN
TITLE OF INVENTION: FII
TITLE OF INVENTION: FOR
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/443,939
FILING DATE: 30-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Schumann, James J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
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APPLICANT: Hajjar, David P.
TITLE OF INVENTION: Treatment of HSV
                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (619)552-1311
TELEFAX: (619)552-0095
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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CITY: Chicago
STATE: Illinois
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                                                                                           STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington
                                                          STATE: Virginia
ZIP: 22202
                                                                                                                                ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 YCKNGGFFLRTHPDGRVDGVREKSD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Schumann, James REGISTRATION NUMBER: 2
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                                                                                                                                                                                                                                                                              Garofano, Luisa
Battistini, Carlo
Carminati, Paolo
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                     SYNERGISTIC COMPOSITION COMPRISING A FIBROBLAST GROWTH FACTOR AND A SULFATED POLYSACCHARIDE, FOR USE AS ANTIVIRAL AGENT
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Pred. No. 0
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US-08-187-780-3
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TELECOMMUNICATION INFORMATION:
TELEPAN: (703)466-2347
TELEPAX: (703)466-2347
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: AMINO ACID
TEORY OF TELETA AMINO ACID
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         FILING DATE: December 6, 1991
APPLICATION NUMBER: 07/177,500
FILING DATE: April 4, 1988
APPLICATION NUMBER: 07/062,92:
FILING DATE: June 16, 1987
ATTORNEY_AGENT INFORMATION:
NAME: HOWARD M. Frankfort
REGISTRATION NUMBER: 32,613
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25
MEDIUM TYPE: 360 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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APPLICANT: DANIELA TALARICO
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ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5288704man F.
REGISTRATION NUMBER: 24,618
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                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/187,780 FILING DATE: January 25, 1994 CLASSIFICATION: 530
                                                                                                                                             APPLICATION NUMBER: 07/901,705
FILING DATE: June 22, 1992
APPLICATION NUMBER: 07/806,771
FILING DATE: December 6, 1991
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 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM or IBM-compatible OPERATING SYSTEM: PC/MS-DOS
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Local Similarity 40.0%;
les 10; Conservative
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                                                                                                                          07/177,506
                                                                                           07/062,925
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                                                                                                                                                                                                                                                                                                                                                                                    5.25 inch,
5986/13586-US3
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Pred. No. 0.19;
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Query Match
Best Local Similarity
****hes 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application Patent No. 5883071 GENERAL INFORMATION:
                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Diskette, 3-
MEDIUM TYPE: 1.44 MB storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,780
                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: ECORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: MAMMALIAN GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CLAUDIO BASILICO APPLICANT: DANIELA TALARICO
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OTHER INFORMATION:
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OTHER INFORMATION:
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TITLE:
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STRANDEDNESS: sin
                                FILING DATE:
                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                             CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOCUMENT NUMBER: FILING DATE:
APPLICATION NUMBER: 0 FILING DATE: June 22,
                                                                                                FILING DATE:
                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                                               10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08478485
                                                                                                                                                                                                                                                                              New York
                                                                                                                                                                                                                                                                                                             805 Third Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (212) 527-7700
               January 25, 1994
UMBER: 07/901,705
                                                                                             Concurrently Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 corresponding to bovine basic fibroblast growth factor, can be found in Table 1, page 9, lines 9, 14, and 19, in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    application, as filed
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                                                                                                              US/08/478,485
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Pred. No. 0.19;
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US-08-478-486F-3
Sequence 3. Application US/08478486F
Patent No. 6432702
GENERAL INFORMATION:
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Best Local 9
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APPLICATION NUMBER: 07/17,5
FILING DATE: April 4, 1988
APPLICATION NUMBER: 07/062,9
FILING DATE: June 16, 1987
ATTORNEY/AGENT INFORMATION:
NAME: Joseph R. Robinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 598
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                       APPLICANT: CLAUDIO BASILICO
APPLICANT: DANIELA TALARICO
TITLE OF INVENTION: MAMMALIAN GRC
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby P.C.
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION METHOD:
OTHER INFORMATION: This sequence,
OTHER INFORMATION: corresponding to bovine basic fibroblast
OTHER INFORMATION: growth factor, can be found in Table 1,
OTHER INFORMATION: page 9, lines 9, 14, and 19, in the
OTHER INFORMATION: application, as filed.
PUBLICATION INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Diskette,
MEDIUM TYPE: 1,44 MB storage
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
DESCRIPTION: Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                      STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                 24 YCKNGGFFLRIHPDGRVDGVREKSD 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: PUBLICATION DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE:
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                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RELEVANT RESIDUES IN SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISSUE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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                                                                                                                                                                                                                  MAMMALIAN GROWTH FACTOR
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07/177,506
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Pred No. 0.19;
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RESULT 11
US-08-231-894A-11
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                                                                                                                                                                                                                             Sequence 11, Application US/08231894A
Patent No. 5851990
GENERAL INFORMATION:
APPLICANT: FUJISHIMA, AKIRA
APPLICANT: FUKUDA, TSUNEHIKO
TITLE OF INVENTION: BEGF MUTEIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/806,771
FILING DATE: December 6, 1991
APPLICATION NUMBER: 07/17,506
FILING DATE: APPLI 4, 1988
APPLICATION NUMBER: 07/062,925
FILING DATE: June 16, 1987
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 753-6237 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA APPLICATION NUMBER: US
                                 ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
FILING DATE: January
APPLICATION NUMBER:
FILING DATE: June 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD:
OTHER INFORMATION: This sequence,
OTHER INFORMATION: corresponding to bovine basic fibroblast
OTHER INFORMATION: growth factor, can be found in Table 1,
OTHER INFORMATION: page 9, lines 9, 14, and 19, in the
OTHER INFORMATION: application, as filed.
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SOFTWARE: Wordper
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REFERENCE/DOCKET NUMBER: 5986/13586-US7
COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                        COUNTRY: US
                                                                                                                          CITY: BOSTON
                                                                                                                                          ADDRESSEE: DAVID G. CONL
ADDRESSEE: 6 CUSHMAN
STREET: 130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                 24 YCKNGGFFLRIHPDGRVDGVREKSD 48
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                                                                                                            STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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June 27, 1954
""MRER: 07/806,771
                                     Diskette
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UMBER: 07/901,705
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Pred. No. 0.19;
5; Mismatches 10; Indels
                                                                                                                                                                              DIKE,
                                                                                                                                                                              BRONSTEIN, ROBERTS
                                                                                                                                                                                                                                   ITS PRODUCTION
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PRIOR APPLICATION DATA:

CURRENT APPLICATION DATA:

SOFTWARE:

FastSEQ Version 1.5

APPLICATION NUMBER: FILING DATE: 22-AP

22-APR-1994

US/08/231,894A

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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NFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
                                                      HYPOTHETICAL: NO
ANTI-SENSE: NO
TYPE: internal
                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                             APPLICANT: FUJISHIMA, AKIRA
APPLICANT: FUKUDA, TSUNEHIKO
TITLE OF INVENTION: BFGF MUTEIN AND ITS PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
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REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION NUMBER: JP 066381-1992
FILING DATE: 24-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                STREET:
APPLICATION NUMBER: US 07/873907 FILING DATE: 24-APR-1992
                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           24 YCKNGGFFLRIHPDGRVDGVREKSD 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                 COUNTRY: US
                                                                                                                                                                                                    STATE:
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5851990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 amino acids
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linear
                                                                                                                                                                                                                                                       DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
                                                                                                                                                                                                                                          & CUSHMAN
                                                                                                                                           Diskette
                                             22-APR-1994
N: 435
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Pred. No. 0.
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US-08-231-894A-13
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; ORIGINAL SOURCE:
US-08-231-894A-12
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Best Local Similarity 40.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617) 523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                              APPLICATION NUMBER: JP 00 FILING DATE: 26-APR-1991 PRIOR APPLICATION DATA:
                                                                                                                                          APPLICATION NUMBER: UFILING DATE: 22-APR-1 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                             SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
ADDRESSEE: 6 CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: FUJISHIMA, AKIRA
APPLICANT: FUKUDA, TSUNEHIKO
TITLE OF INVENTION: BFGF MUTEIN AND ITS PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                                              PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: JP 0
FILING DATE: 26-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                             APPLICATION NUMBER: US 07/873907 FILING DATE: 24-APR-1992 CLASSIFICATION: 435
APPLICATION NUMBER: JP 066381-1992 FILING DATE: 24-MAR-1992
                                                                                                                                                                                                                                                                COMPUTER:
                                                                                                                                                                                                                                                                                                                                                            STREET: 130 V
                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                               ZIP: 02109
                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 YCKNGGFFLRIHPDGRVDGVREKSD 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: RESNICK, DAVID S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 WCTWDAFYLTVHPQGVIEGVRHLVD 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5851990
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                                                                                                                                                                                                                                                                                                                                             MASSACHUSETTS
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                                                                                                                                                                                                                                                                                                                                                                           130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 amino acids
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                                                                                                                                                                                                                                                            IBM Compatible
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                                                                                                                                                                              22-APR-1994
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24-MAR-1992
                                                                                                                                                                                                                                               DOS
                                                                 JP 097655-1991
                                                                                                                                                                                              US/08/231,894A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP 097655-1991
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Pred. No. 0.19;
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HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: 11
ORIGINAL SOURCE:
US-08-231-894A-13
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US-08-231-894A-14
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Best Local Similarity 40.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/08231894A
Patent No. 5851990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: RESNICK, DAYLD 3.

REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 4176
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/231,894A FILING DATE: 22-APR-1994 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/873907 FILING DATE: 24-APR-1992 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617) 523-644
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
          TELEFAX: (617) 523-644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FUJISHIMA, AKIRA
APPLICANT: FUKUDA, TSUNCEHIKO
TITLE OF INVENTION: BFGF MUTEIN AND ITS PRODUCTION
                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 097655-1991
FILING DATE: 26 APR-1991
PRIOR APPLICATION DATA: JP 066381-1992
APPLICATION NUMBER: JP 066381-1992
EILING DATE: 24 MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: ADVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
ADDRESSEE: 6 CUSHMAN
STREET: 130 WATER STREET
                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OLECULE TYPE:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
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                                                                               REFERENCE/DOCKET NUMBER:
                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 WCTWDAFYLTVHPQGVIEGVRHLVD 27
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                                                                                                                RESNICK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 amino acids
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                             523-6440
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                                                                                                            DAVID S
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                                                                                              34235
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                                                                                 41769-FWC
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Pred. No. 0.
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0.19;
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US-08-231-894A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15, Application US/08231894A Patent No. 5851990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                          TELEFAX: (617) 523-64.
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 097655-1991
FILING DATE: 26-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 066381-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                           REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
                                                                                                                                                                                                                      APPLICATION NUMBER: JP 066381-1992
FILING DATE: 24-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/873907
FILING DATE: 24-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
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           MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                             SEQUENCE CHARACTERISTICS:
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APPLICANT: FUKUDA, TSUNEHIKO
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 24-APPLICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM COR
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2
CLASSIFICATION:
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TOPOLOGY: li
                                              TOPOLOGY:
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                                                             STRANDEDNESS:
                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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Local Similarity 40.0%;
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                                                                                            ENGTH:
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                                                                            amino acid
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                                              linear
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) 523-6440
- NO: 15:
                                                           single
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                                                                                                                                                                                             41769-FWC
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Pred. No. 0.19;
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RAGMENT TYPE:

internal

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run on:
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Gapop 10.0 , Gapext 0.5
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181
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2: \sins2\geneseq\geneseq-embl\An198.DAT: *
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5: \sins2\geneseq\geneseq\geneseq-embl\An198.DAT: *
6: \sins2\geneseq\geneseq\geneseq-embl\An198.DAT: *
7: \sins2\geneseq\geneseq\geneseq-embl\An198.DAT: *
8: \sins2\geneseq\geneseq\geneseq-embl\An198.DAT: *
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9: \sins2\geneseq\geneseq\geneseq-embl\An198.DAT: *
10: \sins2\geneseq\geneseq\geneseq-embl\An199.DAT: *
11: \sins2\geneseq\geneseq\geneseq-embl\An199.DAT: *
12: \sins2\geneseq\geneseq\geneseq-embl\An199.DAT: *
13: \sins2\geneseq\geneseq\geneseq-embl\An199.DAT: *
14: \sins2\geneseq\geneseq\geneseq-embl\An199.DAT: *
15: \sins2\geneseq\geneseq\geneseq-embl\An199.DAT: *
16: \sins2\geneseq\geneseq\geneseq-embl\An199.DAT: *
17: \sins2\geneseq\geneseq\geneseq-embl\An199.DAT: *
18: \sins2\geneseq\geneseq\geneseq-embl\An199.DAT: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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146	146	146	148	148	158	181	181	181	181	Score	
80.7	80.7	80.7	81.8	81.8	87.3	100.0	100.0	100.0	100.0	Query Match Length	œ
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22	20	19	20	19	21	20	19	20	19	BB	
AAB98659	AAY30144	AAW57888	AAY30142	AAW57886	AAY70978	AAY17417	AAW53570	AAY17422	AAW53567	ID	
Soybean protein: S	Amino acid sequenc	Japanese artichoke	Amino acid sequenc	Broad bean raffino	Soybean raffinose	Cucumber raffinose	Cucumber raffinose	Cucumber raffinose	Cucumber raffinose	Description	

The present sequence is a cucumber raffinose synthase fragment.

Claim 2; Page 16; 26pp; Japanese.

11/3/3/3/3/3/3/3/3/3/3/3/3/3/3/3/3/3/3/	112 113 115 117 117
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wheat raffinose sy Rice raffinose syn Rosybean raffinose syn Herbicidally activ Rice raffinose syn Corn raffinose syn Corn raffinose syn Soybean raffinose syn Soybean raffinose syn Soybean raffinose syn FGF antagonist bfG FGF antagonist bfG FGF antagonist bfG Immunogenic peptid Fibroblast Growth FGF antagonist bfG Immunogenic peptid Human basic fibrob rhbFGF mutein CS10 rhbFGF mutein CS10 rhbFGF mutein CS10 rhbFGF mutein CI14 Human basic fibrob rhbFGF mutein CI18 Human basic fibrob rhbFGF mutein CI23 rhbFGF mutein CI23 rhbFGF mutein CI23 fibrob rhbFGF mutein CI23	an raffinos acid seque an raffinos eed raffinos rd raffinos cidally act

ALIGNMENTS

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RESULT 1
AAW53567
Raffinose synthase gene - transformed plant
                                     WPI; 1998-264858/24.
                                                                            26-JUL-1996;
26-APR-1996;
                                                                                                          28-APR-1997;
                                                                                                                              07-APR-1998
                                                                                                                                                 JP10084973-A.
                                                                                                                                                                     Cucumis sativus
                                                                                                                                                                                       Cucumber; raffinose synthase; sucrose; galactinol
                                                                                                                                                                                                          Cucumber raffinose synthase residues 215 to 244.
                                                                                                                                                                                                                              06-JUL-1998 (first entry)
                                                                                                                                                                                                                                                   AAW53567;
                                                                                                                                                                                                                                                                     AAW53567 standard; peptide; 30 AA.
                                                        (AJIN ) AJINOMOTO KK.
                                                                            96JP-0198079
96JP-0107682
                                                                                                          97JP-0111124.
                 useful for preparation of raffinose
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RESULT 3
AAW53570
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AAY17422
ID AAY1
DXXXID
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Best Local Similarity
                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Raffinose synthase forms raffinose from sucrose and galactinol, has an optimum pH of 6 to 8 and working temperature of 35 to 40 degrees C, has a molecular weight of 75 to 95 kDa by gel filtration or 90 to 100 kDa by PAGE and SDS-PAGE under reductive conditions and is inhibited by iodoacetamide, N-ethylmaleimide and myoinositol.
                                                                                                                                                                                                                                                                                             The
06-JUL-1998
                      AAW53570;
                                                AAW53570 standard;
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                          of forming raffinose from sucrose and galactinol. The raffinose synthase gene can be used for expression in a plant for the production of raffinose. The raffinose synthase can give raffinose from sucrose and galactinol efficiently. The present sequence represents a raffinose
                                                                                                                                                                                                                                                                                                                    Example 2; Page 21; 37pp; Japanese.
                                                                                                                                                                                                                                                                                                                                           New raffinose synthase gene - for production of raffinose sucrose and galactinol
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-340516/29
                                                                                                                                                                                                                                                                                                                                                                                                                                24-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JP11123080-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cucumis sativus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cucumber raffinose synthase peptide SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY17422;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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les 30; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _
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                                                                                                                                                                                                                                                                                 present invention describes a raffinose synthase, having an forming raffinose from sucrose and galactinol. The raffinose
                                                                                                                         FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC 30
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                                                                                                            FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC
                                                                                                                                                           30;
                                                                                                                                                                                                                                 peptide from cucumber.
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ilarity 100.0%;
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                                                Protein;
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Pred. No. 2.5
); Mismatches
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Pred. No. 2.5e-19;
; Mismatches 0;
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RESULT 4
AAY17417
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Best Local S
Matches 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-264858/24.
N-PSDB; AAV22250.
New raffinose synthase sucrose and galactinol
                                                                                                                                                                                        Cucumis sativus
                                                                                                                                                                                                                                      Cucumber raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Pages 17-20; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raffinose synthase gene - useful for preparation of raffinose in transformed plant % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUL-1996;
26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP10084973-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cucumis sativus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cucumber; raffinose synthase; sucrose; galactinol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cucumber raffinose synthase.
                                   N-PSDB; AAX61238
                                                                                                                    24-OCT-1997;
                                                                                                                                                                  JP11123080-A.
                                                                                                                                                                                                              Raffinose synthase; sucrose; galactinol
                                                                                                                                                                                                                                                             29-JUL-1999
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                                               WPI; 1999-340516/29.
                                                                      (AJIN ) AJINOMOTO KK
                                                                                                                                            11-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 784 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                             (first entry)
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96JP-0107682
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                                                                                              97JP-0292969
                                                                                                                    97JP-0292969
                                                                                                                                                                                                                                      synthase
                                                                                                                                                                                                                                                                                                           Protein;
            gene
                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Pred. No. 1.2e-17;
; Mismatches 0;
            for production
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             of
             raffinose
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                                                                                                                                                                                                                                                The present sequence is a raffinose synthase from clone sfil.pk125.d4 isolated from a soybean immature flower cDNA library sfil. Raffinose synthase is involved in the biosynthesis of raffinose and higher homologues in the raffinose saccharide family from sucrose. The present sequence is useful for reducing the raffinose saccharide content of soybean seeds which improves the nutritional quality of the soy protein products derived from them.
                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 47-49; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids and encoded proteins involved in the biosynthesis raffinose, useful for producing soybean seeds with a reduced racontent and therefore improved nutritional quality -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Allen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-1998;
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                                                                                                                Local Similarity
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FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC
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                                                                                                             87.3%;
86.7%;
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                                                                                                             Score 158;
Pred. No. 2
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Pred. No. 1.2
0; Mismatches
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                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H
                                                                                                             DB 21;
.6e-14;
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.2e-17;
                                                                                                                                  Length 758;
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AAY30142
ID AAY3
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XX Vici
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \begin{array}{c} \texttt{X} \times \texttt{CCCCCCCCXX} \\ \texttt{X} \times \texttt{T} \\ \texttt{T} \\
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Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the broad bean raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides in the host organism or cell is changed. Raffinose oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW57886 standard; Protein; 799
Raffinose synthase; plant; broad bean; sucrose; raffinose.
                                                   Amino acid
                                                                                                  26-OCT-1999
                                                                                                                                               AAY30142;
                                                                                                                                                                                              AAY30142 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Raffinose synthetase; metabolism modification; food additive; gastrointestinal flora; broad bean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Broad bean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW57886;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 FGWCTWDAFYLTVHPEGVREGVKGLVDGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                         1 FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1998-324670/29.
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                                                                                                                                                                                                                                                                                                               FGWCTWDAFYLKVHPKGVWEGVKSLTDGGC
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                                                                                                                                                                                                                                                                                                                                                                                                             24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wantanabe
                                              sequence of a raffinose synthase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         799 AA;
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                (first entry)
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                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                            81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 148; DB 19;
Pred. No. 8.1e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
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RESULT 8
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Best Local S
Matches 24
This sequence is the Japanese artichoke raffinose invention. The raffinose synthetase is capable of
                                 Claim 1; Page 36-38; 44pp;
                                                    New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
                                                                                                                                                                                                   18-DEC-1997;
                                                                                                                                                                                                                                                                  Stachys sieboldii.
                                                                                                                                                                                                                                                                                         gastrointestinal flora; Japanese artichoke.
                                                                                                                                                                                                                                                                                                                        Japanese artichoke raffinose synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a raffinose synthase protein. The sequence is isolated from plant material of broad beans. The protein forms raffinose by complexing alpha(1 to 6) - D-galactosyl hydroxyl group of the 6C of D-glucose residue in sucrose molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New raffinose synthase gene - is prepared from a plant material
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18-DEC-1996;
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                                                                                                  N-PSDB;
                                                                                                             WPI; 1998-324670/29.
                                                                                                                                  0eda
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                                                                                                                                                                                                                        24-JUN-1998
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                                                                                                                                                                                                                                                                                                   Raffinose synthetase; metabolism modification; food additive;
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                                                                                                                                                                                                                                                                                                                                                                   AAW57888;
                                                                                                                                                                                                                                                                                                                                                                                        AAW57888 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                        (SUMO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SUMO ) SUMITOMO CHEM CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                              238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC 30
                                                                                                                                  K, Wantanabe E;
                                                                                                                                                                                                                                                                                                                                                                                                                                              FGWCTWDAFYLKVHPKGVWEGVKSLTDGGC 267
                                                                                                                                                        SUMITOMO CHEM
                                                                                                  AAV40802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 19-21; 40pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   799 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                             (first entry)
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96JP-0338673.
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80.0%;
                                                                                                                                                        CO LTD
                                  English.
                                                                                                                                                                                                                                                                                                                                                                                         587
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.1e-13;
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synthetase producing r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
 e of the
raffinose
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RESULT 10
AAB98659
ID AAB98
XX
AC AAB98
XX

AAB98659 standard;

protein;

AAB98659;

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RESULT 9
AAY30144
ID AAY3
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a raffinose synthase protein. The sequence is isolated from plant material. The protein forms raffinose by complexing alpha(1 to 6). D-galactosyl hydroxyl group of the 6C of D-glucose residue in sucrose molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY30144;
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18-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New raffinose synthase
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    107
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                                                                                       1 FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC 30
FGWCTWDAFYLNVQPHGVMEGVQGLVDGGC 136
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                                                                                                                                                                                                                                                                                                                                                                           587
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                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97JP-0329006.
96JP-0338673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97JP-0342899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plant; sucrose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of a raffinose synthase protein.
                                                                                                                                                                                                                                   80.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene - is prepared from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                                   Score 146; DB 20;
Pred. No. 1.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 146; DB 19;
Pred. No. 1.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            å
    136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plant material
                                                                                                                                                                                                                                                                                    Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      587;
                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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                                                                                                                                                                                             Gaps
                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a mutant protein of raffinose synthase in which at least one aromatic amino acid present at the position of about 1-7 amino acids from the N-terminus is deleted or replaced. The mutant protein can be used for reducing the raffinose oligosaccharide content in a plant body. The present protein from soybean, was used in the present in a plant tody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycine
                                                                                        (SUMO)
                                                                                                                                           18-DEC-1996;
                                                                                                                                                                                        18-DEC-1997;
                                                                                                                                                                                                                                      24-JUN-1998
                                                                                                                                                                                                                                                                                    EP849359-A2
                                                                                                                                                                                                                                                                                                                                    Glycine
                                                                                                                                                                                                                                                                                                                                                                               Raffinose synthetase; metabolism modification; gastrointestinal flora; soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW57887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW57887 standard; Protein; 781 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 18-20; 30pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel mutant protein of raffinose synthase is useful for raffinose oligosaccharide content in a plant body -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JUL-2000; 2000JP-0200571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP2001078783-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SUMO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention
                                           ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-313373/33.
                                                                                                                                                                                                                                                                                                                                    max.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMITOMO CHEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutein;
                                                                                           SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                           raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein:
                                             Wantanabe E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA
ج
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99JP-0196036
                                                                                                                                           96JP-0338673.
                                                                                                                                                                                      97EP-0122417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ဗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 146; DE
Pred. No. 1.56
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 raffinose oligosaccharide reduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                           food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 780;
                                                                                                                                                                                                                                                                                                                                                                                                           additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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RESULT 12
AAY30143
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 Query Match
Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 24
                                                                         The present sequence represents a raffinose synthase protein. The sequence is isolated from plant material. The protein forms raffinose by complexing alpha(1 to 6)- D-galactosyl hydroxyl group of the 6C of D-glucose residue in sucrose molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the soybean raffinose synthetase of the invention. The raffinose synthetase is capable of producing raffinose by combining a D-galactosyl group through an alpha (1-6) bond with a hydroxyl group attached to the carbon atom at position 6 of a D-glucose residue in a sucrose molecule. The DNA can be used to modify metabolism of a host organism by introducing into the host organism or its cell so that the content of the raffinose family oligosaccharides are useful as food additives with beneficial effects on the gastrointestinal flora.
                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 31-34; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid molecule encoding plant raffinose synthetase capable of producing raffinose, used as food additives with beneficial effects on gastrointestinal flora
                                                                                                                                       Claim 8;
                                                                                                                                                              New raffinose synthase gene -
                                                                                                                                                                                          N-PSDB; AAZ10002
                                                                                                                                                                                                     WPI; 1999-511112/43
                                                                                                                                                                                                                                                     28-NOV-1997;
18-DEC-1996;
                                                                                                                                                                                                                                                                                           12-DEC-1997;
                                                                                                                                                                                                                                                                                                                                            JP11215984-A
                                                                                                                                                                                                                                                                                                                                                                     Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                           Raffinose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY30143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY30143 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAV40801
                                                                                                                                                                                                                            (SUMO ) SUMITOMO CHEM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220 FGWCTWDAFYLKVHPSGVWEGVKGLVEGGC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC
 Similarity
24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                       Page 25-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               781 AA;
                                                   781 AA;
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                     97JP-0329006
96JP-0338673
                                                                                                                                                                                                                                                                                           97JP-0342899
                                                                                                                                                                                                                                                                                                                                                                                                                 of a raffinose synthase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                            plant;
                                                                                                                                    40pp;
             80.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.7%;
                                                                                                                                       Japanese
Score 146; DB
Pred. No. 1.5e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            sucrose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 146; DB 19;
Pred. No. 1.5e-12;
2; Mismatches 4
                                                                                                                                                              is prepared
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30
             DB 20;
                                                                                                                                                                from
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                       Length 781;
                                                                                                                                                             plant
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 Indels
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 Gaps
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1 FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC 30

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RESULT 13
AAB49400
 FTT FTT ID
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                                                                                                                                                                                                              В
                                                                                                                                                                                  Matches
                                                                                                                                                                                         Query Match
Best Local
               Location/Qualifiers
Misc-difference 129
       Misc-difference
                                           Brassica napus
                                                        Raffinose synthase;
                                                                       Rapeseed raffinose synthase.
                                                                                      17-JAN-2000
                                                                                                     AAY32075;
                                                                                                                  AAY32075 standard; Protein;
                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                 The present invention provides novel plant promoters which can be used the production of transgenic plants which express genes with desired
                                                                                                                                                                                                                                                       Example 6; Page 24-27; 36pp; English
                                                                                                                                                                                                                                                                     New soybean plant promoters useful for generating transgenic plants with desired properties
                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                           WPI; 2001-104537/12.
N-PSDB; AAC89523.
                                                                                                                                                                                                                                                                                                                Ishige F,
                                                                                                                                                                                                                                                                                                                             (SUMO ) SUMITOMO CHEM CO LTD.
                                                                                                                                                                                                                                                                                                                                            30-APR-1999;
01-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                  27-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                02-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                              EP1048733-A2
                                                                                                                                                                                                                                                                                                                                                                                                           Glycine max.
                                                                                                                                                                                                                                                                                                                                                                                                                         Plant promoter; transgenic plant; desired property.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Soybean raffinose synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB49400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB49400 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220
                                                                                                                                                       220 FGWCTWDAFYLKVHPSGVWEGVKGLVEGGC 249
                                                                                                                                                              1 FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                              781 AA;
                                                                                                                                                                                                                                                                                                                Watanabe E,
                                                                                                                                                                                  Conservative
                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                  2000EP-0108962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                            99JP-0124527.
99JP-0247211.
/note=
              /note= "encoded by GGY"
                                                        rapeseed;
                                                                                                                                                                                        80.7%;
"encoded by GGW"
                                                                                                                                                                                                                                                                                                                Oeda K;
                                                                                                                   572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 781
                                                                                                                                                                                  2;
                                                                                                                                                                                 Score 146; DB 22;
Pred. No. 1.5e-12;
2; Mismatches 4
                                                        transgenic plant.
                                                                                                                   A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽
                                                                                                                                                                                               Length 781;
                                                                                                                                                                                  Indels
                                                                                                                                                                                  0;
                                                                                                                                                                                  Gaps
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 Qy
                                                                                                                                                                                                RESULT 15
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XX
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                                                                                                                                                                   Query Match
Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                          30-APR-1998;
30-APR-1998;
04-DEC-1998;
10-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
Misc-difference 144
       Misc-difference
                            Brassica
                                                         Mustard raffinose synthase.
                                                                        17-JAN-2000
                                                                                      AAY32074;
                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                               Watanabe E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP953643-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 143
                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-593144/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                              27-APR-1999;
                                                                                                                                        13
                                                                                                                                                                    L Similarity
24; Conserv
                                                                                                                                                                                                                                                                                                                                                           AAZ20210
                           juncea
                                                                                                                                                                                               572 AA;
                                                                                                                                                                    Conservative
                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                Oeda K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
148
/note=
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Westar leaf cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see AAZ20207-10) may be used to obtain other raffinose synthase genes by labeled detection or amplification (claimed). These genes may be used to control the levels of raffinose produced in plants. Antisense genes can be used to knock out existing gene activity, and sense genes to increase the level of gene activity. The resulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, providing general health advantages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents rapessed raffinose synthase, a protein that can bind a D-galactosyl group through an alpha(1-6) bond to the hydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. cDNA
                                                                                                                                            Raffinose synthase; mustard; transgenic plant
                                                                                                                                                                                                                                                                                                                                                      AAY32074 standard; Protein; 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; Page 36-38; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New sense and antisense genes, useful for altering the level raffinose in food plants \mbox{\ \ -}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (see AAZ20210) encoding the enzyme was isolated from rapessed cv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SUMO ) SUMITOMO CHEM CO LTD
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98JP-0120551.
98JP-0345590.
98JP-0351246.
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                  Location/Qualifiers 210
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"encoded by ACR"
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1.1e-12;
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                                                                                                                                                                                                                   This sequence represents mustard raffinose synthase, a protein that can bind a D-galactosyl group through an alpha(1-6) bond to the hydroxy group attached to the carbon atom at the 6-position of the D-glucose residue in a sucrose molecule to form raffinose. cDNA (see AAZ20209) encoding the enzyme was isolated from mustard (Brassica juncea) leaf cDNA by PCR. Probes or primers generated from plant raffinose synthase genes (see AAZ20207-10) may be used to obtain other raffinose synthase genes by labeled detection or amplification other raffinose synthase genes by labeled detection or amplification (claimed). These genes may be used to control the levels of raffinose produced in plants. Antisense genes can be used to knock out existing gene activity, and sense genes to increase the level of gene activity. The resulting transgenic plants may be used as a food source to alter the growing conditions for gut enterobacteria, or providing general health advantages.
                                                                                                                            Ouery Match
Best Local Similarity
Matches 24; Conserv
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30-APR-1998;
04-DEC-1998;
10-DEC-1998;
                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 26; Page 29-31; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New sense and antisense genes, useful for altering the level of raffinose in food plants -
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N-PSDB; AAZ20209.
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                                                            218 FGWCTWDAFYLTVNPDGVHKGVKCLVDGGC 247
                                                                             1 FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC 30
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                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oeda K;
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98JP-0120551.
98JP-0345590.
98JP-0351246.
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                                                                                                                                           79.6%;
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                                                                                                                                             Score 144; DB 2
Pred. No. 3e-12;
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Perfect score:
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq
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length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Match
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181
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FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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T46188

C85025

C96599

T01717

E82168

I46711

$00185

A31674

C37360
       AGKBOB
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                     hypothetical prote probable alpha-1,6 fibroblast growth basic fibroblast g hypothetical prote hypothetical prote probable aliphatic hypothetical prote probable ical prote probable nitrate t basic fibroblast g hypothetical prote membrane subunit o unknown protein, 1 S/T protein kinase
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probable seed inhi
Sipl protein - bar
       conserved hypothet s/t protein kinase
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45	44	43	42	41	40	39	38	37	36	3 5	34	33	32	31	30
49	49	49.5	49.5	49.5	50	50	50	50	50	51	51	51	51	51	51.5
27.1	27.1	27.3	27.3	27.3	27.6	27.6	27.6	27.6	27.6	28.2	28.2	28.2	28.2	28.2	28.5
191	79	720	310	243	996	996	381	284	188	1039	225	106	106	106	353
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Н64744	S55456	AF0242	S39592	AC3600	A95228	E98092	T23250	AB0521	AD0533	F71427	AD0798	S52809	S52799	ERAD31	AF2067
yaeD protein - Esc	GAM1 protein - Pla	probable exported	prolyl aminopeptid	cellulase (EC 3.2.	bacteriocin format	cylM protein, cyto	hypothetical prote	AmpE protein (impo	conserved hypothet	hypothetical prote	probable phosphata	hypothetical prote	hypothetical prote	early E3A 12.1K pr	histidinol phospha

ALIGNMENTS

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probable imbibition protein - wild cabbage
C;Species: Brassica oleracea (wild cabbage)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
C;Accession: S45033
R;Fujikura, Y; Karssen, C.K.
submitted to the EMBL Data Library, May 1994
A;Description: Cauliflower CDNA encoding a putative imbibition protein.
A;Reference number: S45033
A;Accession: S45033
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S45033
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                                                                                                                                                   C;Genetics:
A;Gene: sip
                                                                                                                                                                                    A;Cross-references: EMBL:X95875; NID:g1212811
A;Experimental source: germinating seed
                                                                                                                                                                                                      A:Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-357 <CER>
A;Cross-references: EMBL:X95875; NID:g1212811
                                                                                                                                                                                                                                                                                  A; Reference number: A; Accession: T09530
                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, February 1996 A; Reference number: 216718
                                                                                                                                                                                                                                                                                                                                            C; Accession:
R; Cervantes,
                                                                                                                                                                                                                                                                                                                                                              probable seed inhibition protein - chickpea (fragment)
C;Species: Cicer arietinum (chickpea, garbanzo)
C;Date: 16-Jul-199 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C;Accession: T09530
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A; Residues: 1-765 < FUJ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                           T09530
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                                                                     Query Match
Best Local Similarity 62.1
Matches 18; Conservative
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Best Local
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31
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nes 19; Conserv
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FGWCTWDAFYTDVTAEGVEEGLKSLSEGG
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Pred. No. 2.
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Pred. No. 2.3e-07;
3; Mismatches 7;
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                                                                                           DB 2;
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A; Molecule type: DNA
A; Residues: 1-807 <STO>
                                                                                                 A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana A;Reference number: A85001; MUID:20083488; PMID:10617198 A;Accession: C85025
                                                                                                                                                                                               hypothetical protein AT4g01970 [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 C:Accession: C85025
                    A;Cross-references: GB:NC_001268; NID:g7268581; PIDN:CAB80690.1;
                                                                                 A;Status: preliminary
                                                                                                                                                             R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprir Nature 402, 769-777, 1999
                                                                                                                                                                                                                                                                                                                                                                 β
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A; Residues: 1-773 <BEN>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         imbibition protein homolog - Arabidopsis thaliana
N;Alternate names: protein T8H10.120
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Species: Hordeum vulgare (barley)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Sep-1997
C:Accession: S27762
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C;Spe
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A; Accession: T46188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: R; Benes, V.;
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A; Residues: 1-757 <HEC>
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        Genetics:
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Best Local
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18; Conser

    barley

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62.1%;
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Library, February 1992
Characterization of a gene,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 108; DB Pred. No. 5.9e 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   489/3;
                                                                                                                                                                                                                                                                                                                                                                                                     29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No. 6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ansorge, W.; Mewes, H.W.; Lemcke, K.; ase, January 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; 1
5.9e-07;
hes 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 773,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 757;
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                        GSPDB:GN00140
                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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QΥ
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RESULT 7
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                                                                              A; Introns: 5/2; 25/3; A; Note: A_IG002N01.5
                                                                                                                                              A: Experimental source: cultivar Columbia C: Genetics:
                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein A_IG002N01.5 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Decies: Arabidopsis thaliana (mouse-ear cress) C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 24-Mar-1999 C;Accession: T01717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1170 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein F20N2.14 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                       A; Map position: 4
                                                                                                                                                                                 A;Cross-references: EMBL:AF007269; NID:g2191126; PID:g2191156
                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-371 <SCH>
                                                                                                                                                                                                                                           A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                A; Reference number: A; Accession: T01717
                                                                                                                                                                                                                                                                                     A; Description: The sequence A; Reference number: 214407
                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, June 1997 A; Description: The sequence of A. thaliana IG002N01
                                                                                                                                                                                                                                                                                                                                                   R;Scheet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE005173; NID:g8778496; PIDN:AAF79504.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A86141; A; Accession: C96599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Theologis, A.; Ecker, J.R.; Palm, Chin, C.W.; Chung, M.K.; Conn, L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 4
      Matches
                                           Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 FGWCTWDAFYTNVTAKDVKQGLESNCD 229
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      Local Similarity
nes 11; Conser
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                                                                                                                                                                                                                                                                                                                                            P.; Maggi, L.
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      Conservative
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                                                                                                   103/3; 126/1; 174/2;
                        39.8%;
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62.1%;
      0;
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                        Score 72; DB 2;
Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 106;
Pred. No. 1.
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Conway, A.B.; Conway, A.
Mismatches
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                                                                                                     240/1;
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. 0.0039;
                                           DB 2;
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.2e-06;
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                                                                                                   284/1; 295/1;
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    2,
                                         Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1170;
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    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaul,
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                                                                                                     333/2;
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    0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Khaykin, E.; Kim,
Maiti, R.; Marzia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
    Gaps
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    0;
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1 FGWCTWDAFYLTV

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A;Title: Primary structure of ovine pituitary basic fibroblast growth factor A;Reference number: S00185; MUID:88055577; PMID:3678486 A;Accession: S00185
                                                                                                                          C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 C;Accession: S00185
                                                                                                                                                                             basic fibroblast growth factor - sheep N;Alternate names: prostatropin C;Species: Ovis orientalis aries, Ovis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Winkles, J.A.; Friesel, R.; Alberts, G.F.; Janat, M.F.; Liau, Am. J. Pathol. 143, 518-527, 1993
A:Title: Elevated expression of basic fibroblast growth factor A:Reference number: 146711; MUID:93343209; PMID:8342599
A:Accession: 146711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fibroblast growth factor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 16-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Heldelberg, J.F.; Elsen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwir Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; l, R.R.; Mckalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
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C;Accession: E82168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable alpha-1,6-galactosidase VC1690 [imported] - Vibrio cholerae (strain N16961 serc
C;Species: Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                      R;Simpson, R.J.; Moritz, R.L.; Lloyd, C.J.; Fabri, FEBS Lett. 224, 128-132, 1987
                                                                                                                                                                                                                                                    S00185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-137 <WIN>
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A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-374 <HEI>
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  A; Molecule type:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                     WCTWDAFYLTVHPQGVIEGVRHLVD 27
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protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 60; DB 2; Length 137; Pred. No. 0.47; 5; Mismatches 10; Indels
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                                                                                                              L.J.; Nice, E.C.; Rubira, M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9,
                                                                                                                                                          #text_change
                                                                                                                                                                                  (domestic sheep)
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H.; Dragoi, I.; Sellers,
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                                                                                                                Burge
                                                                                                                                 C; Species: Mus musculus (house mouse)
C; Date: 17-Apr-1993 #sequence_revision
C; Accession: C37360
                       A; Title: Isolation of cDNAs encoding four mouse FGF family members A; Reference number: A37360; MUID:90201563; PMID:2318343 A; Accession: C37360
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                                                                                      R; Hebert, J.M.; Basilico, C.;
Dev. Biol. 138, 454-463, 1990
                                                                                                                                                                                                  basic fibroblast growth factor - mouse
  A;Status: preliminary
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basic fibroblast growth factor precursor - rat
N;Alternate names: bFGF
C;Species: Rattus norvegicus (Norway rat)
C;Species: 1-May-1990 #sequence_revision 21-May-1990 #text_change 16-Jul-1999
C;Accession: A31674; S00876; S24309
C;Accession: A31674; S00876; S24309
                                                                                                                                                                                                                                                                                                                                                                            A:Cross-references: EMBL:X07285; NID:g56203; PIDN:CAA30265.1; R;El-Husseini, A.E.D.; Paterson, J.A.; Myal, Y.; Shiu, R.P.C. Biochim. Biophys. Acta 1131, 314-316, 1992
A;Title: PCR detection of the rat brain basic fibroblast growt A;Reference number: $24309; MUID:92329546; PMID:1378302
A;Accession: $24309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M22427; NID:g204285; PIDN:AAA41210.1; R;Kurokawa, T.; Seno, M.; Igarashi, K. Nucleic Acids Res. 16, 5201, 1988
A;Title: Nucleotide sequence of rat basic fibroblast growth fa;Reference number: S00876; MUID:88262516; PMID:3387229
A;Accession: S00876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Keywords: growth factor; heparin binding; mitogen E;18-22/\text{Region}: heparin binding *status predicted E;107-110/\text{Region}: heparin binding *status predicted
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C:Superfamily: fibroblast growth factor
                                                                                                                                                                                                          C;Keywords: growth factor F;1-9/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                               A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 35-154 <ELH>
A;Cross-references: EMBL:X61697; NID:g56143; PIDN:CAA43863.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Shimasaki, S.; Emoto, N.; Koba, A.; Mercado, M.; Shibata, F.; Cooksey, K.; Baird Biochem. Biophys. Res. Commun. 157, 256-263, 1988 A;Title: Complementary DNA cloning and sequencing of rat ovarian basic fibroblast A;Reference number: A31674; MUID:89061721; PMID:3196337
                                                                                                                                                                                      F;10-154/Product: basic fibroblast growth factor #status
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A; Residues: 1-154 < KUR>
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A; Residues: 1-154 <SHI>
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17-Apr-1993 #text_change 16-Jul-1999

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Regul. Pept. 16, 135-145, 1986
A, Title: Purification and partial characterization of a mitogenic factor A; Reference number: A60310; MUID:87119165; PMID:3809608
A; Accession: A60310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 16-35 <BER)
R;Ueno, N.; Baird, A.; Esch, F.; Ling, N.; Guillemin, R.
Mol. Cell. Endocrinol. 49, 189-194, 1987
Mol. Tible: Isolation and partial characterization of basic fibroblast growth factor from A;Reference number: A61551; MUID:87162856; PMID:3556754
A;Accession: A61551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: pituitary gland R; A; Mergia, A; Fiddes, J.C. R; Abraham, J.A.; Whang, J.L.; Tumolo, A.; Mergia, A.; Fiddes, J.C. Cold Spring Harb. Symp. Quant. Biol. 51, 657-668, 1986 A; Title: Human basic fibroblast growth factor: nucleotide sequence, A; Reference number: A90924; MUID:87217066; PMID:3472745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Bos primigenius taurus (cattle)
C;Date: 13-Aug-1986 #sequence_revision 02-Jun-1995 #text_change 24-Nov-1999
C;Accession: A24663; A32878; A33784; A61550; A61551; A60310; A61094; A01386; ¿R;Abraham, J.A.; Mergia, A.; Whang, J.L.; Tumolo, A.; Friedman, J.; Hjerrild, Science 233, 545-548, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Isolation, characterisation and tissue localisation A;Reference number: A61550; MUID:87247652; PMID:3596000 A;Accession: A61550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 3-157 <AB2>
R;Residues: 3-157 <AB2>
R;Milner, P.G.; Li, Y.S.; Hoffman, R.M.; Kodner, C.M.; Siegel, N.R.; Deuel,
Biochem. Biophys. Res. Commun. 165, 1096-1103, 1989
A;Title: A novel 17 kD heparin-binding growth factor (HBGF-8) in bovine uter
A;Reference number: A33784; MUID:90121211; PMID:2610682
A;Accession: A33784
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A; Residues: 1-154 <HEB>
A; Cross-references: GB: M30644; NID:g193296;
                                                                                                                                                          A;Molecule type: protein
A;Residues: 23-35,'X',37-42 <UEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 27-35, 'X', 37-41 <UE3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Bertolini, J.; Hearn, M.T.W. Mol. Cell. Endocrinol. 51, 187-199, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein A; Residues: 1-14 <MIL>
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A; Residues: 3-157 < ABR>
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Experimental source: liver; Ling, N.; Guillemin, R.; Ueno, N.; Baird, A.; Esch, F.; Ling, N.; Guillemin, R.; Commun. 138, 580-588, 1986 iochem. Biolation of an amino terminal extended form of Fille: Isolation of an amino terminal extended form of Reference number: A24819; MUID:86295737; PMID:3741423
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A;Experimental source: adrenal gland R;Esch, F.; Baird, A.; Ling, N.; Ueno, N.; Hill, F.; Denoroy, L.; Klepper, R.; Gospod Proc. Natl. Acad. Sci. U.S.A. 82, 6507-6511, 1985
A;Title: Primary structure of bovine pituitary basic fibroblast growth factor (FGF) a A;Reference number: A01386; MUID:86016731; PMID:3863109
A;Accession: A01386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Superfamily: fibroblast growth factor

C; Superfamily: fibroblast growth factor: hep

F; 1-157/Product: basic fibroblast growth factor, blocked amino end; growth factor; hep

F; 1-157/Product: basic fibroblast growth factor, pituitary gamma form #status experim

F; 12-157/Product: basic fibroblast growth factor, pituitary alpha form #status experim

F; 12-157/Product: basic fibroblast growth factor, pituitary short form #status predic

F; 23-157/Product: basic fibroblast growth factor, pituitary short form #status predic

F; 27-157/Product: basic fibroblast growth factor, hepatic form #status experimental 

F; 27-157/Product: basic fibroblast growth factor, renal form #status experimental 

F; 29-33,118-121/Region: heparin binding #status predicted

F; 4/Modified site: blocked amino end (Ala) (in mature form pituitary gamma) (probably
                                                                                                                                          C:Species: Homo sapiens (man)
C:Date: 31-Jul-1989 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000
C:Date: 31-Jul-1989 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000
C:Accession: A32398; A61537; A26642; B32878; S00297; A54316; B54316; A33624;
R:Prats, H.; Kaghad, M.; Prats, A.C.; Klagsbrun, M.; Lelias, J.M.; Liauzun, E
Proc. Natl. Acad. Sci. U.S.A. 86, 1836-1840, 1989
A:Title: High molecular mass forms of basic fibroblast growth factor are init
A:Reference number: A32398; MUID:89184522; PMID:2538817
A:Accession: A32398
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A; Mesidues: 12-26 <BOH>
A; Residues: 12-26 <BOH>
C; Comment: The acidic and basic fibroblast growth factors are the major endothelial-c
ell types in vitro (although bFGF is 30-100 times more potent than aFGF in stimulatin
C; Comment: This protein binds heparin more strongly than does aFGF.
A;Cross-references: GB:J04513; NID:g183083; R;Shibata, F.; Baird, A.; Florkiewicz, R.Z.
                                                                         A; Residues: 1-210 < PRA>
                                                                                                              A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                basic fibroblast growth factor precursor, 22.5K form N;Alternate names: bFGF; fibroblast growth factor 2; N;Contains: basic fibroblast growth factor, 18K form
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A;Title: Isolation and partial molecular characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Accession: A60316
A;Molecule type: protein
A;Residues: 27-35', X', 37-43 <BAI>
A:Experimental source: kidney
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A; Title: Isolation and partial characterization of an endothed A; Reference number: A60316; MUID:86095426; PMID:4081126
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A;Note: the amino end of this form was blocked; the peptide composition matched what R;Gospodarowicz, D.; Baird, A.; Cheng, J.; Lui, G.M.; Esch, F.; Bohlen, P. Endocrinology 118, 82-90, 1986
A;Title: Isolation of fibroblast growth factor from bovine adrenal gland: physicochem A;Reference number: A61094; MUID:86081530; PMID:3940857
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R;Abraham, J.A.; Whang, J.L.; Tumolo, A.; Mergia, A.; Frie
EMBO J. 5, 2523-2528, 1986
A;Title: Human basic fibroblast growth factor: nucleotide
A;Reference number: S00297; MUID:87053817; PMID:3780670
A;Accession: S00297
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A;Residues: 56-210 <KUD>
A;Residues: 56-210 <KUD>
A;Residues: 56-210 <KUD>
A;Cross-references: GB:M27968; NID:g182562; PIDN:ANA52448.1; PID:g18
A;Cross-references: GB:M27968; NID:g182562; PIDN:ANA52448.1; PID:g18
Cold Spring Harb. Symp. Quant. Biol. 51, 657-668, 1986
Cold Spring Harb. Symp. Quant. Biol. 51, 657-668, 1986
A;Title: Human basic fibroblast growth factor: nucleotide sequence,
A;Reference number: A90924; MUID:87217066; PMID:3472745
A;Accession: B32878
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A;Title: Cloning and expression of cDNA encoding human l A;Reference number: A26642; MUID:87162468; PMID:2435575
A;Accession: A26642
                             FEBS
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R;Gimenez-Gallego, G; Conn, G; Hatcher, V.B.; Thomas, F
Biochem. Biophys. Res. Commun. 135, 541-548, 1986
A;Title: Human brain-derived acidic and basic fibroblast
A;Reference number: A90122; MUID:86186784; PMID:3964259
                                                                                                                                                                                                                                                                                                                                                                                             R;Story, M.T.; Esch, F.; Shimasaki, S.; Sasse, J.; Jacobs, S.C.; Biochem. Biophys. Res. Commun. 142, 702-709, 1987
A;Title: Amino-terminal sequence of a large form of basic fibrobl A;Reference number: A25824; MUID:87156686; PMID:2435284
A;Accession: A25824
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J. Cell Biol. 109, 3105-3114, 1989
J. Title: Differential effects of heparin, f
A;Reference number: A33624; MUID:90078343;
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 'XX',86-88,'X',90-91,'X',93-95 <SH3>
A;Residues: 'XX',86-88,'X',90-91,'X',93-95 <SH3>
A;Reseldues: 'XX',86-88,'X',90-91,'X',93-95 <SH3>
A;Reseldues: 'XX',86-88,'X',90-91,'X',93-95 <SH3>
A;Recellues: 'XX',86-88,'X',90-91,'X',93-95 <SH3>
A;Accession: B54316
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A;Residues: 1-155 <AB2>
A;Rote: the authors translated the codon GAA for residue 108 as Gly
A;Note: the authors (Gotoh, M.; Ino, Y.; Sakamoto, M.; Kato, K.; Hirohashi, S.
R;Shimoyama, Y.; Gotoh, M.; Ino, Y.; Sakamoto, M.; Kato, K.; Hirohashi, S.
Jpn. J. Cancer Res. 82, 1263-1270, 1991
A;Title: Characterization of high-molecular-mass forms of basic fibroblast
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                                                                               A;Molecule type: protein
A;Residues: 65-102,'X',104-105 <GIM>
A;Experimental source: brain
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A; Residues: 'XXX', 19, 'X', 21-29 <SH2>
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A; Residues: 1-155 < Al
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                                                                                                                                                                 A; Reference number: A90122; A; Accession: B24243
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R;Felge, J.J.; Bradley, J.D.; Fryburg, K.; Farris, J.; Cous
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                          P.; Frater-Schroder, M.; Bohlen,
204, 203-207, 1986
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of endothelial cell mitogens
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A; Molecule type: mRNA
A; Residues: 54-210 <SOM>
A; Residues: 54-210 <SOM>
A; Cross-references: EMBL:M17599; NID:g183086; PIDN:AAA52534.1; PID:g183087
A; Pantoliano, M.W.; Horlick, R.A.; Springer, B.A.; Van Dyk, D.E.; Tobery, 'Blochemistry 33, 10229-10248, 1994
Blochemistry 33, 10229-10248, 1994
A; Title: Multivalent ligand-receptor binding interactions in the fibroblas: A; Reference number: A55784; MUID:94347757; PMID:7520751
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A;Accession: B24301
A;Molecule type: protein
A;Residues: 65-88,'X',90-98,'X',100 <GAU>
R;Sommer, A.; Brewer, M.T.; Thompson, R.C.; Moscatelli, D.; P
Biochem. Biophys. Res. Commun. 144, 543-550, 1987
A;Title: A form of human basic fibroblast growth factor with
A;Reference number: S42242; MUID:87213238; PMID:3579930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Start codon: CTG
C;Superfamily: fibroblast growth factor
C;Superfamily: fibroblast growth factor; angiogenesis; growth factor; heparin binding;
C;Keywords: alternative initiators; angiogenesis; growth factor, 18K form #status predicted <MAN2
F;1-210/Product: basic fibroblast growth factor, 18K form #status predicted <MAN2
F;85-210/Product: basic fibroblast growth factor, 18K form #status predicted
F;82-86/Region: heparin binding #status predicted
F;171-174/Region: heparin binding #status predicted
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A:Residues: 54-71 <PAN>
A:Residues: 54-71 <PAN>
R:Watson, R.; Anthony, F.; Pickett, M.; Lambden, P.; Masson,
Biochem. Biophys. Res. Commun. 187, 1227-1231, 1992
A:Title: Reverse transcription with nested polymerase chain
submitted to the EMBL Data Library
A;Reference number: Z19830
A;Accession: T24018
A;Status: preliminary; translated
                                                                                                               hypothetical protein R07B7.11 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change C;Accession: T24018
R;Harris, B.
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A; Status: preliminary
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A; Title: Purification and characterization of the 210-amino acid recombinant basic A; Reference number: S46253; MUID:94320639; PMID:8045296
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A;Map position: 4q25-4q27
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A; Residues: 39-53;65-88 <PAT>
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Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE AN
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Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast growth factor) (BFGF) (Prostatropin).
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            33.1%;
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                                                    WW.
5.
            Score 60;
Pred. No.
                                                                 HEPARIN (POTENTIAL).
                                                                                          HEPARIN-BINDING GROWTH FACTOR
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Sciurognathi; Muridae
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                                                    689F677416274388 CRC64;
 Mismatches
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            0.21;
                          DB 1;
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10;
                       Length 154;
Indels
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ng embryogenesis.";
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RESULT 3
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ID FGF2
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              EMBL;
                                                                                                                                                                                                                                            El-Husseini A.E.-D., Paterson J.A., Myal Y., Shiu R.P.C.;
"PCR detection of the rat brain basic fibroblast growth factor (
mRNA containing a unique 3' untranslated region.";
Biochim. Blophys. Acta 1131:314-316(1992).

-i- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC
IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES
VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND
CONCENTRATION OF THESE 2 GROWTH FACTORS.

-i- SUBUNIT: MONOMER.

-i- TISSUE SPECIFICITY: FOUND IN ALL THE TISSUES EXAMINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FGF2_RAT
P13109;
                                                                         modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast growth factor) (BFGF) (Prostatropin).
                                 EMBL;
                                                                                                                                       the
                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Sprague-Dawley; TISSUE-Brain; MEDLINE-92329546; PubMed-1378302;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 35-154 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Rasumarthi K.B.S., Jin Y., Cattini P.A.;
"Cloning of the rat ribroblast growth factor-2 promoter its response to mitogenic stimuli in glioma C6 cells.";
J. Neurochem. 68:898-908(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Sprague-Dawley; TISSUE-Testis. MEDLINE-97200905; PubMed-9048734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kurokawa T., Seno M., Igarashi K.; "Nucleotide sequence of rat basic fibroblast growth factor cDNA."; Nucleic Acids Res. 16:5201-5201(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Sprague-Dawley; TISSUE=Ova MEDLINE=89061721; PubMed=3196337;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-28 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=88262516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complementary DNA cloning and sequencing of rat ovarian basic fibroblast growth factor and tissue distribution study of its mRNA."; Blochem. Biophys. Res. Commun. 157:256-263(1988).
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                                                                                                                       European Bioinformatics Institute. The by non-profit institutions as long
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M22427;
X07285;
U78079;
X61697;
                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL
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CAA30265.
AAC53225.
CAA43863.
                                              AAA41210.1;
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SEQUENCE OF 1-9.

MEDILINE-86295737; PubMed-3741423;

Ueno N., Baird A., Esch F., Ling N., Guil

"Isolation of an amino terminal extended
growth factor.";

Biochem. Biophys. Res. Commun. 138:580-58
                                                                                                                                       SEQUENCE OF 10-155.

MEDLINE-86016731: PubMed-3863109;

ESCh F., Baird A., Ling N., Ueno N., Hill F., Denoroy L., Kleppe Gospodarowicz D., Boehlen P., Guillemin R.;

"Primary structure of bovine pituitary basic fibroblast growth f (FGF) and comparison with the amino-terminal sequence of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
23-OCT-1986 (Rel. 02, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Heparin-binding growth factor 2 precursor (HBGF-2) (Basic fibroblast growth factor) (BFGF) (Prostatropin) [Contains: Kidney-derived growth
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MEDLINE-86261806; PubMed-2425435;
Abraham J.A., Mergia A., Whang J.L., Tumolo A.,
Hjerrild K.A., Gospodarowicz D., Fiddes J.C.;
"Nucleotide sequence of a bovine clone encoding
protein, basic fibroblast growth factor.";
Science 233:545-548(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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23-OCT-1986
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Growth factor;
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ProDom; PD000831; HB/F_growt
SMART; SM00442; FGF; 1.
SMART; SM00247; HBGF_FGF;
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InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
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"Human basic fibroblast growth factor:
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A31674.
                                                                                                                                                                                                                                                            fibroblast growth factor: nucleotide sequence, and expression in mammalian cells."; arb. Symp. Quant. Biol. 51:657-668(1986).
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   Commun. 138:580-588(1986).
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                                                                                                                 82:6507-6511(1985).
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Baird A., Esch F., Boehlen P., Ling N., Gospodarowicz D.;
"Isolation and partial characterization of an endothelial cell growth
factor from the bovine kidney: homology with basic fibroblast growth
factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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-IF FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND CONCENTRATION OF THESE 2 GROWTH FACTORS.

-I- SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91095983; PubMed=1702556; Zhu X., Komiya H., Chirino A., Faham S., Hsu B.T., Rees D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Kidney:
MEDLINE-87119165; PubMed-3809608;
Ueno N., Baird A., Esch F., Shimasaki S., Ling N., Guillemin R.;
"Purification and partial characterization of a mitogenic factor
"Purification and partial characterization of a mitogenic factor
bowine liver: structural homology with basic fibroblast growth
factor.":
                                                                                                                                                                                    STRAND
                                                                                                                                                                                                                                                                                                                                                                                    Growth factor; Mitogen;
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InterPro; IPR002348; IL1_HBGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MISCELLANEOUS:
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CELL ATTACHMENT SITE (POTENTIAL)
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MEDLINE-87217066; PubMed=3472745;

MEDLINE-87217066; PubMed=3472745;

Abraham J.A., Whang J.L., Tumolo A., Mergia A., Fiddes J.C.;

Pluman basic fibroblast growth factor: nucleotide sequence,

"Human basic fibroblast growth factor: nucleotide sequence,

"Human basic fibroblast growth factor: nucleotide sequence,

organization, and expression in mammalian cells ";

organization, and expression in biol. 51:657-668(1986).
   growth
FEBS Le
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M.T., Thompson
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Science
MEDLINE=97040521; PubMed-8885834; Moy F.J., Seddon A.P., Boehlen P., Powers R.; Moy F.J., Seddon Structure of basic fibroblast growth : "High-resolution solution structure of basic fibroblast growth determined by multidimensional heteronuclear magnetic resonance
                                                            STRUCTURE
                                                                                                                                                 MEDLINE=91095983; PubMed=1702556; Zhu X., Komiya H., Chirino A., Fa
                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
MEDLINE=92121151; PubMed=1769963;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Eriksson A.E., Cousens L.S., Matthews B.W.; "Refinement of the structure of human basic at 1.6-A resolution and analysis of presumed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Story M.T., Esch F., Shimasaki S., Sasse J., Jacobs S.C., "Amino-terminal sequence of a large form of basic fibrobl factor isolated from human benign prostatic hyperplastic Biochem. Biophys. Res. Commun. 142:702-709(1987).
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MEDLINE=89184522; PubMed=2538817; Prats H., Kaghad M., Prats A.C., | Prats D.P., Chalon P., Tauber J.P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     x-ray crystallography (1.6 angstroms)
MEDLINE=94004464; PubMed=7691311;
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MEDLINE=91195367; PubMed=1707542;
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SEQUENCE FROM
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acad. Sci. U.S.A. 86:1836-1840(1989)
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of human basic
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EMBL; J04513; AAA52533.1; ALT_INIT.
PIR; A25824; A26642.
PIR; A25824; A26642.
PIR; B24301; B24301.
PIR; B24301; B24301.
PIR; B32878; B32878.
PIR; B32878; B32878.
PIR; S00297; S00297.
PDB; JFCG; 15-JUL-93.
PDB; JFCG; 15-JUL-93.
PDB; JFCG; 15-JUL-93.
PDB; JFCG; 15-JUL-93.
PDB; JFCG; 15-JUN-97.
PDB; JFCG; 03-APR-96.
PDB; JFCG; 31-JAN-94.
PDB; JFCG; 31-JAN-94.
PDB; JFCG; 31-JAN-94.
PDB; JFCG; 18-KGC; FCC.
PDB; JFCG; 18-KGC; FCC.
                                                                                                                                                                           BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute or the European Bioinformatics Institute. There are no the European Bioinformatics Institute. There are no the European Bioinformatics Institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed.
           HELIX
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SITE
SITE
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                                                                                                                                                                                                                                                                   PRINTS; PR00262; ILHBGF.
PRODOMS; PD000831; HB/F_growthfact;
SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF_FGF; 1.
                                                                                                                                                                                                                                                                                                                   InterPro: IPR002209; HB/F_growthfact.
InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                spectroscopy.";
Biochemistry 35:13552-13561(1996).
-!- FUNCTION: THE HEPARIN-BINDING
                                                                                                                                                                                                                                   PROPEP
                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:3676; FGF2
                                                                                                                                                                                                                                               3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIGGENIC IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES CUTRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND CONCENTRATION OF THESE 2 GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: MONOMER.
Angiogenesis;
                                                                                                                                                                         HEPARIN-BINDING GROWTH FACTOR 2.
CELL ATTACHMENT SITE (POTENTIAL)
CELL ATTACHMENT SITE (POTENTIAL)
HEPARIN (POTENTIAL).
HEPARIN (POTENTIAL).
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RESULT 6
FGF2_SHEEP
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01-FEB-1996 (Rel. 3, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2002 (Rel. 41, Last annotation update)
18-JUN-2002 (Rel. 41, Last annotation update)
18-JUN-2002 (Rel. 17, Created)
18-JUN-
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Sutton R., Ward W.G., Re
Submitted (SEP-1994) to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovidae; Caprinae;
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
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                  InterPro; IPR002209; HB/F_growthfact.
InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
                                                                                          EMBL; L36136; PIR; S00185; S
                                                                                                                                                   or send an
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PRINTS; PR00262;
                                                                          HSSP; P09038; 1BFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tactor
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                                                                                                                                                                                                                                                                                                                                              S Lett. 224:128-132(1987).

FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIGGENIC FUNCTION: THE POPENT MITOGENS FOR A VARIETY OF CELL TYPES IN TIRE. ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND CONCENTRATION OF THESE 2 GROWTH FACTORS.

SUBUNIT: MONOMER.

MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN
                                                                                                                                                                                                                                                                                                          AFGF. SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through
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10; Conser
                                                                                                                                                                                       non-profit institutions as long and this statement is not removed.
                                                                                                                                                   requires a license agreement (san email to license@isb-sib.ch)
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IL1HBGF
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co the EMBL/GenBank/DDBJ databases
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RESULT 7
FGF2_MONDO
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Best Local
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BINDING
SEQUENCE
                                                                           InterPro; IPR002209; HB/F_growthfact.
InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Heparin-binding growth factor 2 precursor (HBGF-2) (Basic growth factor) (BFGF) (Prostatropin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Growth
PROPEP
CHAIN
SITE
BINDING
                                                         PRINTS; PR00262; IL1HBGF.
ProDom; PD000831; HB/F_growthfact;
                                                                                                              EMBL; Z15154; CAA78
HSSP; P09038; 1BFF
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                             Growth factor;
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                                                 SMART; SM00442; FGF;
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                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=13616;
                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                               Monodelphis
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                                                                                                                                                                          European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
                                                                                                                                                                                                                                                  MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN
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                                       PS00247; HBGF_FGF;
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155 AA;
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Metazoa; Chordata; Craniata; Vertebrata;
etatheria; Didelphimorphia; Didelphidae;
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                                                                                                                        CAA78854.1; ALT_INIT.
                            Mitogen;
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90 C
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119 H
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40.0%;
                  Angiogenesis; Heparin-binding BY SIMILARITY.
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Pred.
HEPARIN-BINDING GROWTH FACTOR HEPARIN (POTENTIAL).
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CELL ATTACHMENT SITE
HEPARÎN (POTENTIAL).
HEPARÎN (POTENTIAL).
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0.21;
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Monodelphis.
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ALT_INIT

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RESULT 8
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P75853; Q9R7Q5;
15-JUL-1998 (Rel. 3
15-DEC-1998 (Rel. 3
16-OCT-2001 (Rel. 4
                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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SEQUENCE
                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sampei G., Seki Y.,
Yano M., Horiuchi T
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kinura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Salto N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _ECOLI
                                                                                                                                                                                                                                                                                                                                          "A 718-kb DNA Sequence of Escherichia coli K-12 Genome Corre to the 12.7-28.0 mln Region on the Linkage Map."; DNA Res. 3:137-155(1996).
-i- FUNCTION: PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
STRAIN-K12 / MG16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The Escherichia coli ssuEADCB gene cluster is required for the utilization of sulfur from aliphatic sulfonates and is regulated the transcriptional activator Cbl.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97061202; PubMed=8905232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mau B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99436146; PubMed=10506196;
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                                                                                                                                                                                                                                                                 ALIPHATIC SULFONATES. PUTATIVE BINDING PROTEIN. SUBCELLULAR LOCATION: Periplasmic (Potential). SIMILARITY: TO B.SUBTILIS SSUA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete genome sequence of Escherichia coli K-12.", nce 277:1453-1474(1997).
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  AJ237695;
AE000195;
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9; Conser
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CAB40390.1;
AAC74022.1;
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37, Last sequence update)
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17303 MW;
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7E655FCC49BF1209 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bykowski T., Hryniewicz M.,
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P48800;
     BINDING
BINDING
SEQUENCE
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Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       growth factor) (BFGF). FGF2 OR FGF-2.
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Transport; Periplasmic; Signal; Complete proteome SIGNAL 1 21 POTENTIAL.
CHAIN 22 319 PUTATIVE ALIPHATIC SU
                                                                                                                                 SMART; SM00442; FGF; 1.
PROSITE: PS00247; HBGF FGF. 1
STOWTH fact.
                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no. way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borja A.Z., Zeller R., Meijers C.; "Expression of alternatively spliced brgr first antisense mRNAs during chicken embryogenesis."; Dev. Biol. 157:110-118(1993).
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Heparin-binding growth factor 2 precursor (
                                                                                                       PROPEP
                                                                                                                                                                                                     PRINTS; PR00262; IL1HBGF. ProDom; PD000831; HB/F_gr
                                                                                                                                                                                                                                                     Pfam; PF00167; FGF; 1.
                                                                                                                                                                                                                                                                                                                          EMBL; M95707; AAA48617.1;
HSSP; P09038; 1BFF.
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MEDLINE=93246053; PubMed=7683281;
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InterPro; IPR001638; SBP_bac_3.
SMART; SM00062; PBPb; 1.
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                                                                                                                                                                                                                                                                          InterPro; IPR002209; HB/F_growthfact.
InterPro; IPR002348; IL1_HBGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND CONCENTRATION OF THESE 2 GROWTH FACTORS.

SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFGF.
SIMILARITY: BELONGS TO THE HEPARIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: MONOMER.
MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN MORE STRONGLY THAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WAIWDPYYSAALLQG---GVRVLKDG 202
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                              Mitogen; Angiogenesis; Heparin-binding.

1 12 BY SIMILARITY.
3 158 HEPARIN-BINDING GROWTH FA.
4 HEPARIN (POTENTIAL).
9 122 HEPARIN (POTENTIAL).
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Neognathae; Galliformes; Phasianidae;
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RESULT 10
PTP6_DROME
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InterPro; IPR003598; IQ_C2.
InterPro; IPR003598; Ig_C2.
InterPro; IPR00360; Ig_like.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; TYR_PP.
Pfam; PF00041. fr
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Best Local
         Pfam; PF00041; fn3; 3.

pfam; PF001012; Y_phosphatase; 2.

pfam; PF001102; Y_phosphatase; 2.

Pfam; PF001102; Y_phosphatase; 2.

PRINTS; PR00700; PRTYPHPHTASE.

SMART; SM00400; Fn3; 3.

SMART; SM00410; IG_11ke; 1.

SMART; SM00410; IG_12k; 1.

SMART; SM00194; PTPC; 2.

SMART; SM00194; PTPC; 2.

PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.

PROSITE; PS00055; TYR_PHOSPHATASE_2; 2.

PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.

Hydrolase; Receptor; Glycoproteln; Signal; Cell adhesion; Immunoglobulin domain; Rep

SIGNAL

1 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
the Europ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-90046860; PubMed-2554325;
Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;
"A family of receptor-linked protein tyrosine phosphatases and Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1990 (Rel.
01-AUG-1990 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;

Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brach

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                     EMBL; M27699; AAA288
PIR; B36182; B36182.
HSSP; P18052; 1YFO.
                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removentities requires a license agreement (Son send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
-i- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-i- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
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01-AUG-1990 (Rel. 15, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protein-tyrosine phosphatase DPTP precursor (EC
                                                                                                                                                                                                                                                                                                                        FlyBase; FBgn0014007;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 86:8
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                                                                                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tyrosine + phosphate.
SUBCELLULAR LOCATION: Type I membrane
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9; Conser
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86:8698-8702(1989).
THAT DPTP IS A CELL ADHESION RECEPTOR
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                                       Transmembrane;
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PROTEIN-TYROSINE

PHOSPHATASE DPTP

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QBYV89;
15-JUN-2002 (Rel. 41, 0
15-JUN-2002 (Rel. 41, 1
15-JUN-2002 (Rel. 41, 1
                                                                                                                                                                                                                           _ANASP
    cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8.205-213(2001).
-!- CATALYTIC ACTIVITY: L-histidinol-phosphate + 2-oxogl
(imidazol-4-yl)-2-oxopropyl phosphate + L-glutamate.
-!- COFACTOR: Pyridoxal phosphate (By similarity).
-!- PATHWAY: Histidine biosynthesis; seventh step.
                                                                    MEDLINE-21595285; PubMed-11759840; Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.
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CARBOHYD
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ACT_SITE
DISULFID
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TRANSMEM
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Nakazaki N., Snamm
Nakazaki N., Tabata
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DOMAIN
                                             "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                SEQUENCE FROM N.A.
                                                                                                                               Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales;
NCBI_TaxID=103690;
                                                                                                                                                          HISC1 OR ALR2092.
                                                                                                                                                                 acetol-phosphate transaminase 1).
                                                                                                                                                                        15-JUN-2002 (Rel. 41, Last annotation update)
Histidinol-phosphate aminotransferase 1 (EC 2.6.1.9) (Imidazole
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Last annotation updat
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FIBRONECTIN TYPE-III 2.
PROTEIN-TYROSINE PHOSPHATASE 1
PROTEIN-TYROSINE PHOSPHATASE 2
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                            6;
                                                                                                                                                                                                                                                                                           Score 52; DB
Pred. No. 24;
6; Mismatches
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N-LINKED
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CYTOPLASMIC (POTENTIAL)
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IG-LIKE C2-TYPE DOMAIN 2.
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                                                                                                                                         Nostocaceae; Nostoc.
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                             2-oxoglutarate =
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Query Match
Best Local s
Matches
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Best Local :
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01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update
01-AUG-1992 (Rel. 23, Last annotation update
probable early E3 12.1 kDa glycoprotein.
Human adenovirus type 3.
Viruses; dsDNA viruses, no RNA stage; Ader
NCBL_TaxID-45659;
                                                                                                   PIR;
                                                                                                                                                                                                                                                                                   adenovirus-3 and the non-oncogenic adenovirus-2.";
Gene 50:173-184(1986).
                                                                          Early protein; Glycoprotein. CARBOHYD 77 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADE03
                                                            SEQUENCE
                                                                                                                    EMBL; M15952;
                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its the EMPL of the EMPL of the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                         Signaes C., Akusjaervi G., Pettersson 
"Region E3 of human adenoviruses; diff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Histidine biosynthesis; Transferase; Aminotransferase; Pyridoxal phosphate; Complete proteome.
BINDING 211 211 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AP003588; BAB73791.1;
Interpro; IPR004839; Aminotransf1/2.
Interpro; IPR001917; Wittransf 2.
Pfam; PF00155; aminotran_1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                     SERE SUCLIVE TO THE KNOWN.

-!- FUNCTION: NOT YET KNOWN.

-!- SIMILARITY: TO EQUIVALENT PROTEIN IN OTHER ADENOVIRUSES.
                                                                                                                                                                                                                                                                                                                                                  MEDLINE=87219876; PubMed=3582978;
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGREAMS; TIGRO1141; hisc; 1.
PROSITE; PS00599; AA_TRANSFEE_CLASS_2;
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P_NEIGO STANDARD;
P42786;
01-NOV-1995 (Rel. 32, Cr
01-NOV-1995 (Rel. 32, La
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                                                                               YAED_ECOLI
P31546;
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SEQUENCE
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   Escherichia
                           Hypothetical YAED OR B0200
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ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z25461; CAA80948.1; -. HSSP; O32449; 1QTR.
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Bacteria; Proteobacteria;
NCBI_TaxID=485;
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Microbiol. 9:1203-1211(1993)
FUNCTION: HYDROLYSES PEPTIDES HAVING THE
YIELD FREE PROLINE. ALSO HYDROLYSES THE C
CATALLYTIC ACTIVITY: Release of a N-termin
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                        OR B0200
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Pred. No. 12;
7; Mismatches
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PROTON DONOR (BY SIMILARITY).
DOE7AEBA908A1AEO CRC64;
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli colol?:H7 and genomic comparison with a laboratory strain K-12."; DNA RES. 8:11-22(2001).

DNA RES. 8:11-22(2001).

-i- SIMILARITY: STRONG, TO H.INFLUENZAE HI0621.1.

-i- SIMILARITY: TO M.JANNASCHII MJ0015.
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Davis K., Federspiel
Lashkari D., Lew H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takemoto K., Mori H., Murayama N., Kataoka K., Yano M., Itoh T. Yamamoto Y., Inokuchi H., Miki T., Hatada E., Fukuda R., Ichiha Mizuno T., Makino K., Nakata A., Yura T., Sampei G., Mizobuchi "Systematic sequencing of the Escherichia coli genome: analysis 4.0 - 6.0 min (189,987 - 281,416bp) region."; Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
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Blattner F.R., Plunkett G. III, Bloch C./
Riley M., Collado-Vides J., Glasner J.D.,
Gregor J., Davis N.W., Kirkpatrick H.A.,
                                                                                                                                                                                                                                                                                                                          STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
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MEDLINE=21074935; PubMed=11206551;
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This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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"Development of primer sets for direct sequence
the ribosomal operons of Escherlchia coll.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ da
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-0157:H7 / RIMD 0509952;
Ohnishi M., Murata T., Nakayam
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STRAIN-K12 / W3110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miyamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia
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                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science
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                                                                 PHOSPHATE PHOSPHATASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete genome sequence ce 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proteobacteria;
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Lin
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N., Hyman R.,
Lin D., Namath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakayama K.,
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R., Kalman S., K
math A., Oefner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli K-12.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.A., Perna N.T., Burland V.,
.D., Rode C.K., Mayhew G.F.,
A., Goeden M.A., Rose D.J.,
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S., Komp C., Kurd
fner P., Roberts I
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1 H., Hayash
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                                                                                            THE HISTIDINOL
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                                                                                                                                                                                                                                                        Yasunaga
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Tobe T.,
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                                                                                                                                                                                                                                                                                                                                                                                       RX KEDLINE-77061201; PubMed-8905231;
RX KADENCE-77061201; PubMed-8905231;
RA KADEKO T. Sato S. KOCANI H., TANAKA A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
RA Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
RA Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
RA Miyajima N., Matsuno A., Muzaki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
Yamada M., Yasuda M., Tabata S.;
RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
Yamada M., Yasuda M., Tabata S.;
RA Yamada M., Yasuda Y., Watanabe A.,
Yasuda T., Watana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPB001455; Hlgnase/hydrlase.
InterPro; IPR004446; Hstdl_phs_rel.
Pfam; PF00702; Hydrolase; I.
TIGRFAMS; TIGR00213; hstdl_phs_rel; 1.
Hypothetical protein; Complete proteom
SEQUENCE 191 AA; 21294 MW; E7814B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                         EMBL; D90915;
                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; AE005195; AAG54502.1; -.
EMBL; AP002550; BAB33625.1; -.
ECOGene; EG11736; yaeD.
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EMBL; AE000129; AAC73311.1; -.
   InterPro;
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                                                                                                                                                                                                                                                    European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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   IPR004143;
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                                     BAA18623.1;
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28.6%;
BPL_LipA_LipB
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3; Mismatches
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E7814B34A23128FA CRC64;
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Job time : 5.93902 secs
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Best Local
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                                                                                                                                                SEQUENCE
                                                                                                                                                                                               Pfam; PF03099; BPL_LipA_LipB; 1
ProDom; PD006086; Lipoate_B; 1.
                                                                                                                                                Ligase; Complete proteome. SEQUENCE 227 AA; 25640 MW;
                                                                                                                                                                                                                      InterPro; IPR000544; Lipoate_B.
                                                150 GWVTCHGFALNICPD--LEGFSHIVPCG
                                                                        2 GWCTWDAFYLTVHPQGVIEGVRHLVDGG
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            27,
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Result
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Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maximum
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SP_Barchea:*

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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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      of hits satisfying chosen parameters:
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181
1 FGWCTWDAFYLTVF
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84.5
791.2
791.6
64.6
661.3
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sp_bacteria:*
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sp_virus:*
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sp_rvirus:*
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Q9SBZ0
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Q93XK2
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Q94607
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Q94007
Q94008
Q94408
Q95YJ4
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Q942T6
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Compugen Ltd.
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09zt62 cucumis sativ
0942t6 oryza sativ
08vwn6 pisum sativ
09fnd9 arabidopsis
08rw08 stachys aff
09sbz0 phaseolus a
043408 brassica ol
09sbz0 phaseolus a
043408 brassica ol
093466 cicer ariet
040077 hordeum vul
09scm1 arabidopsis
094408 arabidopsis
094408 arabidopsis
09syj4 arabidopsis
09syj4 arabidopsis
09mx87 arabidopsis
09mx87 arabidopsis
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ALIGNMENTS

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Q942T6
Q942T6;
Q1-DEC-2001
01-DEC-2001
01-DEC-2001
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09ZT62;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohsumi C., Nozaki J., Kida T.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF073744; AAD02832.1;
Glycosyltransferase; Transferase.
SEQUENCE 784 AA; 86920 MW; 3B06A491F0908933 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cucumis sativus (Cucumber).

Cukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
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TISSUE-LEAF;
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                                                                                                                                                                                                                                                                                                         FGWCTWDAFYLTVHPQGVIEGVRHLVDGGC
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   l (TrEMBLrel. 19,
l (TrEMBLrel. 19,
l (TrEMBLrel. 19,
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                                                                                                                                          PRELIMINARY;
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Created)
Last sequence update)
Last annotation update)
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Pred. No. 7e-17;
Mismatches
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O9FND9 PRELIMINARY; PRT; 783 A
O9FND9;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence
O1-JUN-2002 (TrEMBLrel. 21, Last annotatio
Raffinose synthase protein.
RMPO12.13.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; eudicotyledo
eurosids II; Brassicales; Brassicaceae; Ar
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Q8VWN6;
01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pisum sativum (Garden pea).
Eukaryota; Viridiplantae; Stre
Eukaryota; Magnoliophyta;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transferase; Glycosyltransferase.
SEQUENCE 798 AA; 88717 MW; 8E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CV. WUNDER VON KELVEDON; TISSUE-SEED;
Peterbauer T., Mach L., Mucha J., Richter A.;
"Molecular characterization of raffinose synt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eurosids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
Raffinose synthase (EC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases EMBL; AP003282; BAB64768.1; -. SEQUENCE 816 AA; 89588 MW; B316EDF3566C5178 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P0583G08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3888;
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80.0%;
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2.4.1.82).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ha J., Richter A.;
of raffinose synthase from pea
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Pred. No. 4.
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Pred. No. 6.
                          eudicotyledons;
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                            core eudicots;
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Matches 24
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Submitted (NOV-2001) to the survey of the su
                                                                                          "Molecular cloning of a cDNA enco
Stachys sieboldii.";
Submitted (AUG-2001) to the EMBL/
EMBL; AJ344091; CAC86963.1; -
Transferase; Glycosyltransferase.
SEQUENCE 863 AA; 95227 MW; DR
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachec Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Lamiaceae; Stachys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carnincí P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Scker J., Theologis A., Davis R.W.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AB006702; BAB11595.1; -. EMBL; AY081645; AAM10207.1; -. EMBL; AY081645; AAM10207.1; -.
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                                                                                                                                                                                                                                                        TISSUE=LEAF;
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01-JUN-2002
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                                                                                                                                                                                                                                 Pesch M., Schmitz K.;
                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=168825;
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MEDLINE=98069011; PubMed=9405937;
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Pred. No. 1.1e-11;
3; Mismatches 3
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MEDLINE-20117502; PubMed-10652123;

MEDLINE-20117502; PubMed-10652123;

Peterbauer T., Mucha J., Mayer U., Popp M., Glo

"Stachyose synthesis in seeds of adzuki bean (V

molecular cloning and functional expression of

plant J. 20:509-518(1999)

EMBL; Y19024; CAB64363.1; -

GlyCOSYLtransferase; Transferase.

SEQUENCE 857 AA; 94949 MW; 85248C4B81165679
                                                                                                                                                                                                                                                                                                                           Q43408
Q43408;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
093XK2;
093XK2;
01-DEC-2001
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01-MAY-2000 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Galactinol-raffinose galactosyltransferase (EC 2.4.1.67).
Phaseolus angularis (Adzuki bean) (Vigna angularis; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
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                                                                                                                                                                                                                                                                     Putative imbibition protein.

Brassica oleracea (Cauliflower).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN-CV. ALPHA BALOMA; TISSUE-ROOT TIPS;
Fujikura Y., Karssen C.K.;
"Cauliflower cDNA encoding a putative imbibition protein.";
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; X79330; CAA55893.1; ...
                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                            NCBI_TaxID=3712;
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
  (TrEMBLrel.
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94949 MW; 85248C4B81165679
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Pred. No. 4.5e
3; Mismatches
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Pred. No. 7.4e-08;
4; Mismatches 6
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Q40077;
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Q1-NOV-1996
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids I; Fabales; Fabaceae; Papilionoideae; Cicereae; Cicer.
NCBI_TaxID-3827;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
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Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Str.
Spermatophyta; Magnoliophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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18; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39465 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.7%;
62.1%;
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                                                                                                                            01,
01,
19,
Streptophyta; En
yta; Liliopsida;
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Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 108;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 111;
Pred. No. 5
                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E8CD30399E1BF3EE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                          757
  Embryophyta; Tracheophyta;
a; Poales; Poaceae; Pooldea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10
.1e-07
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.2e-07
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; Vicieae; Pisum.
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     Pooideae;
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RESULT OF CONTRACT OF CONTRACT
   RESULT 12
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CO EUGAT
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Best Local S
Matches 18
                                                                                                                 094A08 PRELIMINARY; PRT; 773 AA.

Q94A08;

01-DEC-2001 (TrEMBLrel. 19, Created)

r 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

r 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

Putative imbibition protein.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; T.

Spermatophyta; Magnoliophyta; eudicotyledons; core eud eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(NCBL_TaxID-3702;
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Q9SCM1;
CPENBLEEL 13, CF
O1-MAY-2000 (TEMBLEEL 13, LF
O1-MAY-2000 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Best I
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SEQUENCE FROM N.A. Yamada K., Liu S.X., I Goldsmith A.D., Jiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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Submitted (FEB-1992) to the EMBL/GenBank/DDBJ
EMBL; M77475; AAA32975.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triticeae; Hordeum NCBI_TaxID=4513; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EU Arabidopsis sequencing project;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ
EMBL; AL133248; CAB66109.1; -
SEQUENCE 773 AA; 85143 MW; 0852F9E67952C8E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Benes V., Rechmann S., Borko
Mayer K.F.X., Quetier F., Sa
Submitted (NOV-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Imbibition protein T8H10.120.
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Heck G.R., Dorse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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"Cloning and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200
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18; Conser
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18; Conser
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   Pham P.
g P.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HO T.-H.D.;
ization of a gene, Sipl, associated
   Lee
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Last annotation updat
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Pred. No. 1.2e
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EA9E7B771AABBCCF
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   Banh J., Banno
J.M., Onodera (
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1.2e-06;
8;
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1.2e-06;
7;
                                                                                                                                                                                          embryophyta; Tracheophyta
edons; core eudicots; Rosi
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   Dale J.
                                                                                                                                                                                             eudicots; Rosidae;
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RESULT 14
Q9M4M7
ID Q9M4N
AC Q9M4N
DT 01-0C

Q9M4M7 Q9M4M7; 01-OCT-2000 01-OCT-2000

(TrEMBLrel.

15, 15,

Created)

sequence update;

PRELIMINARY;

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RESULT 13
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PRELIMINARY;

PRT; 807 AA.

C Q9SYJ4;

C Q9SYJ4;

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T 01-MAY-2000 (TrEMBLrel. 13, Created)

T 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

T 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)

Putative raffinose synthase OR seed IMBIBITION protein.

N T7B11.23 OR AYAGO1970.

S Arabidopsis thaliana (Mouse-ear cress).

C Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trac

C Spermatophyta; Magnoliophyta; eudicotyledons; core eudic

C eurosids I; Brassicales; Brassicaceae; Arabidopsis.

N NCBL_TaxID=3702;
                                                                                                                                                                                                             SEQUENCE FROM N.A.

Spiegel L.A., Huang E.N., Nascimento
Spiegel L.A., Matero A., Shah R., O'Shaughnessy
Preston R.R., Matero A., Shah R., O'Shaughnessy
Shekher M., Schutz K., See L.H., Swaby I., Habo
Shekher M., Schutz K., Mayer K.F.X.;
Mewes H.W., Lemcke K., Mayer K.F.X.;
Mewes H.W., Lemcke K., Mayer K.F.X.;
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                                                                                                                                                                                                                                                                                                                                            Huang E.N., Nascimento L., de la Bastide M., Hak
Preston R.R., Spiegel L.A., See L.H., Shah R., M
O'Shaughnessy A., Rodriguez M., Shekher M., Swat
Parnell L.D., Dedhia N.N., McCombie W.R.;
"Arabidopsis thallana BAC T7B11 from Chromosome
Submitted (APR-1999) to the EMBL/GenBank/DDBJ da
                                                                                                                        EU Arabidopsis sequencing pr
Submitted (MAR-2000) to the
EMBL; AC007138; AAD22659.1;
EMBL; AL161493; CAB80690.1;
SEQUENCE 807 AA; 90122 MW
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Synthase OR seed IMBIBITION protein.
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62.1%;
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Shah R., O'Shaughnessy &
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Pred. No. 1.
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Q8RX87;
O1-JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
AT5920250/F5024_140.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN-CV. HASS; TISSUE-MESOCARP;

Zamorano J.P., Evans A.D., Dopico B., Lowe A.L., Wilson I.D.,

Merodio C., Grierson D.;

"Isolation and characterization of cDNAs for mRNAs regulated during
cold storage of avocado (Persea americana Mill.) fruit.";

Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ133148; CAB77245.1;

EMBL; AJ133148; CAB77245.1;

SEQUENCE 779 AA; 85368 MW; C3ABB43160316785 CRC64;
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                                                                                                                                                                                                                                                                                    Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J., Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G. Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Persea.
NCBI_TaxID=3435;
                                                                                                                                                                                                    "Arabidopsis cDNA clones.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY090237; AAL90901.1; -.
SEQUENCE 844 AA; 94215 MW; 2AC8AB0EA43F8056 CRC64;
                                                                                                                                                                                                                                                                           Ecker J.R.;
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203 FGWCTWDAFFTDVTDEGVEEGLKSLSGGG 231
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                                                                 FGWCTWDAFYQEVTQEGVEAGLKSLAAGG
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17; Conservative
               27,
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4; Mismatches
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Pred. No. 2.4e-05;
3; Mismatches 9
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1: /cgn2_6/ptodata/2/pubpaa/U
2: /cgn2_6/ptodata/2/pubpaa/U
3: /cgn2_6/ptodata/2/pubpaa/U
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181
1 FGWCTWDAFYLTVF
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US-09-940-601-3
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US-10-108-195-4
US-10-108-195-7
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0 US-09-808-958-9
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RESULT 2 US-09-940-601-3 ; Sequence 3, Application US/09940601 ; Publication No. US20030004319A1	Qy Db 1	Query M Best Lo Matches	RESULT 1 US-09-901-938 Sequence 24 Patent No. GENERAL INE APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: CURRENT EN CURRENT		20 20 22 22 22 23 24 24 25 33 33 34 44 44 44 44 44 44 44 44 44 44
	aatch 33 cal Similarity 40. 10; Conservative WCTWDAFYLTVHPQGVIEC : : : : CKNGGFFLRIHPDGRVDG	atc} cal	100 238		51 53 600 600 600 600 600 600 600 600 600 60
		$\alpha \vdash$	-24 , Application US US20020156001A1 ORMATION: ECONS, Michael ECONS, Michael WHITE, Kenneth STROM, Tim WEITINGER, Tho WEITINGER, Tho NVENTION: NOVEL ENCE: 053884-500 PLICATION NUMBER LING DATE: 2000-07 ICATION NUMBER: NG DATE: 2000-07 SEQ ID NOS: 34 PatentIn version 4 HOMO Sapiens -24	0 3 0	200 200 200 200 200 200 200 200 200 200
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		Length 134; ; Indels 0; Gaps	(FGF23) AND METHODS FOR		Sequence 6, Appli Sequence 10, Appl Sequence 10, Appli Sequence 6, Appli Sequence 6, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 6, Appli Sequence 10116, A Sequence 10116, A Sequence 11714, A Sequence 17, Appli Sequence 1, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 7, Appli
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SSD

GENERAL INFORMATION:
APPLICANT: Basilico, Claudio
APPLICANT: Delli Bovi, Pasquale
TITLE OF INVENTION: MAMMALIAN GROWTH FACTOR
FILE REFERENCE: 5986/13586-USC
CURRENT APPLICATION NUMBER: US/09/940,601

PRIOR APPLICATION NUMBER: 08/ PRIOR FILING DATE: 1996-12-31

2001-08-27 3ER: 08/775,567

CURRENT FILING DATE:

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US-10-131-965-3
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APPLICANT: Whitehouse, Martha J.
APPLICANT: Kavanaugh, Michael W.
                                                                                                                                                               Sequence 5, Application US/10131965
Patent No. US20020165160A1
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 10; Conserv
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APPLICANT: Whitehouse, Martha J.
APPLICANT: Kavanaugh, Michael W.
TITLE OF INVENTION: Angiogenically Effect:
TITLE OF INVENTION: Administering
FILE REFERENCE: 1296/12169US905
CURRENT APPLICATION NUMBER: US/10/131,965
CURRENT FILING DATE: 2002-04-25
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CURRENT APPLICATION NUMBER: US/10/131,965
CURRENT FILING DATE: 2002-04-25
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PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 15
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PRIOR FILING DATE: 1988-04-04
PRIOR APPLICATION NUMBER: 07/062,925
PRIOR FILING DATE: 1987-06-16
NUMBER OF SEQ ID NOS: 8
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PRIOR EILING DATE: 1991-12-06
PRIOR APPLICATION NUMBER: 07/177,506
PRIOR FILING DATE: 1988-04-04
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TYPE: PRT
ORGANISM: Bos taurus
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40.0%;
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                                                                                  Effective Unit Dose of FGF and Method of
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; TYPE: PRT
; ORGANISM: bovine FGF-2
US-10-131-965-5
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APPLICANT: Kwan, Chi-Pong
APPLICANT: Wenkataraman, Ganesh
APPLICANT: Shriver, Zachary
                                                                                                                                                                                                                                            Sequence 3, Application US/10108195 Publication No. US20030008820A1
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LENGTH: 146
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FILE REFERENCE: M00656/70076
CURRENT APPLICATION NUMBER: US/10/108,195
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 60/279,165
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 15
                                                                                                              \begin{array}{lll} & \texttt{APPLICANT:} & \texttt{Sasisekharan,} & \texttt{Ram} \\ & \texttt{TITLE OF INVENTION:} & \texttt{Methods} & \texttt{and} & \texttt{Products} & \texttt{Related} \\ \end{array}
                                                                                                                                                   APPLICANT:
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PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 15
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CURRENT FILING DATE: 2002-03-27
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APPLICANT: Raman, Rahul
APPLICANT: Sasisekharan, Ram
TITLE OF INVENTION: Methods and Products Related to
FILE REFERENCE: M00656/70076
CURRENT APPLICATION NUMBER: US/10/108,195
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 60/279,165
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
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US-10-108-195-4
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US-10-108-195-3
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US-10-108-195-4
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Best Local Similarity 40...
10; Conservative
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Publication No. US20030008820A1
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Best Local Similarity
                                                                                                            APPLICANT: Shriver, Zachary
APPLICANT: Raman, Rahul
APPLICANT: Sasisekharan, Ram
TITLE OF INVENTION: Methods and Products Related
FILE REFERENCE: M00656/70076
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APPLICANT: Venkataraman, Ganesh
APPLICANT: Shriver, Zachary
CURRENT APPLICATION NUMBER: US/10/108,195
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 60/279,165
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
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APPLICANT: Venke
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TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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Pred. No. 0.55;
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; OTHER INFORMATION: Native FGF2 with 9 N-terminal Residues Deleted US-10-108-195-7
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APPLICANT: Whitehouse, Martha Jo
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Best Local Similarity 40.0
Matches 10; Conservative
                                                                                                                                           SEQ ID NO 4
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Best Local
                  Query Match
Best Local
     Matches
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CURRENT APPLICATION NUMBER: US/09/802,365
CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/188,480
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/203,415
                                                                                                                                                                                         TITLE OF INVENTION: Methods and Compositions for the TITLE OF INVENTION: Treatment and Prevention of Erectile Dysfunction FILE REFERENCE: 1671.003
CURRENT APPLICATION NUMBER: US/09/802,365
CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/188,480
PRIOR PILING DATE: 2000-03-10
PRIOR PILING DATE: 2000-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Whitehouse, Martha Jo
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Treatment and Prevention of Erectile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-05-11
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                            NUMBER OF SEQ ID NOS: 9 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                         ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
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                                                                                                           TYPE: PRT
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                                                                                                                      LENGTH:
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   l Similarity
10; Conserv
33.1%;
milarity 40.0%;
Conservative
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Pred. No. 0.55;
 Score 60; DB 10;
Pred. No. 0.55;
5; Mismatches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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     10;
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Indels

Gaps

WCTWDAFYLTVHPQGVIEGVRHLVD

27

US-09-886-856-4

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RESULT 13
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; ORGANISM: Bos taurus
US-09-886-856-2
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US-09-886-856-2
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US-09-771-302-2
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Best Local Similarity
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Patent No. US20020115603A1
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Patent No. US20020072489A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Whitehouse, Martha Jo
TITLE OF INVENTION: Methods and Compositions
TITLE OF INVENTION: Treatment of Peripheral
FILE REFERENCE: PP16090.004
CURRENT APPLICATION NUMBER: US/09/886,856
CURRENT FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 60/213,504
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                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/276,549
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Whitehouse, Martha J.

TITLE OF INVENTION: Anglogenically Effective Unit Dose of FGF-2 and Method
TITLE OF INVENTION: Of Use
FILE REFERENCE: 1296/12169US04
CURRENT APPLICATION NUMBER: US/09/771,302
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/385,114
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/104,102
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEO ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/264,572 PRIOR FILING DATE: 2000-01-26
                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                 LENGTH: 146
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                                                          24 YCKNGGFFLRIHPDGRVDGVREKSD 48
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; Pred. No. 0.55
5; Mismatches
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                                                                                                                                                        DB 10; Length 146;
0.55;
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US-09-820-596-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens US-09-886-856-4
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LENGTH: 146
TYPE: PRT
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/213,504
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/264,572
PRIOR FILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: 60/276,549
PRIOR FILING DATE: 0008-01-276,549
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TITLE OF INVENTION: Methods and Compositions
TITLE OF INVENTION: Treatment of Peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/886,856
CURRENT FILING DATE: 2001-06-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL
                                                                                 INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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mes 10; Conserv
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                 APPLICATION NUMBER: 09/036,594
FILING DATE: CURKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Arnold E., Beth
REGISTRATION NUMBER: 35,430
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/820,596 FILING DATE: 29-Mar-2001 PRIOR APPLICATION DATA:
                                                                                                                                                                        REFERENCE/DOCKET NUMBER: MIA-026.01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL INFORMATION:
APPLICANT: Khodadoust, Mehran Mohammad
TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTORS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FastSEQ for Windows Version 4.0
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
STATE: MA
                                           TYPE: amino acid
                                                                                                                               TELEFAX: 617-832-7000
                                                                                                                                                 TELEPHONE: 617-832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                             LENGTH: 147 amino acids
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                    <Unknown>
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Pred. No. 0.
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APPLICANT: KITSCHOET, MAIC W.
APPLICANT: KITSCHOET, WO. US20020090651Allyukl
TITLE OF INVENTION: Receptor-Ligand Assay
FILE REFERENCE: H095-01A2
CURRENT APPLICATION NUMBER: US/10/016,447
CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/08/776,207
PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-23
PRIOR FILING DATE: EARLIER FILING DATE: 1995-05-15
PRIOR PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1995-05-15
PRIOR FILING DATE: EARLIER FILING DATE: 1995-05-15
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1994-07-22
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 150
TYPE: PRT
ORGANISM: Homo sapien
US-10-016-447-8
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US-10-016-447-8
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Search completed: March 27, 2003, 10:20:35 Job time: 6.95122 secs
                                                                                                                                                                                        Query Match 33.1%;
Best Local Similarity 40.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/10016447
Patent No. US20020090651A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 33.1%; Score 60; DB 9; Length 147; Best Local Similarity 40.0%; Pred. No. 0.55; Matches 10; Conservative 5; Mismatches 10; Indels
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25 YCKNGGFFLRIHPDGRVDGVREKSD 49
                                                                                            33 YCKNGGFFLRIHPDGRVDGVREKSD 57
                                                                                                                          3 WCTWDAFYLTVHPQGVIEGVRHLVD 27
                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                               Score 60; DB 12; Length 150; Pred. No. 0.56;
                                                                                                                                                                                           10; Indels
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